DEC 1 8 2002 EN PRADEMINA

SEQUENCE LISTING

GENERAL INFORMATION:

- (i) APPLICANT: ALBERTSEN, HANS
 ANAND, RAKESH
 CARLSON, MARY
 GRODEN, JOANNA
 HEDGE, PHILIP J.
 JOSLYN, GEOFF
 KINZLER, KENNETH
 MARKHAM, ALEXANDER F.
 NAKAMURA, YUSUKE
 THLIVERIS, ANDREW
- (ii) TITLE OF INVENTION: INHERITED AND SOMATIC MUTATIONS OF APC GENE IN COLORECTAL CANCER IN HUMANS
- (iii) NUMBER OF SEQUENCES: [102] 154
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Banner & Allegretti, LTD
 - (B) STREET: 1001 G Street, NW
 - (C) CITY: Washington
 - (D) STATE: D.C.
 - (E) COUNTRY: USA
 - (F) ZIP: 20001-4598
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 07/741,940
 - (B) FILING DATE: 08-AUG-1991
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Kagan, Sarah A.
 - (B) REGISTRATION NUMBER: 32,141
 - (C) REFERENCE/DOCKET NUMBER: 1107.035574
 - (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 202-508-9100
 - (B) TELEFAX: 202-508-9299
- (2) INFORMATION FOR SEQ ID NO:1:

	STRANDEDNESS: do FOPOLOGY: linear			
(ii) MOLECU	ULE TYPE: cDNA			
	NAL SOURCE:			
(A) (ORGANISM: Homo s	apiens		
· ,	IATE SOURCE: CLONE: DP2.5(APC)		
(ix) FEATUR				
•	NAME/KEY: CDS LOCATION: 3485	62		
(xi) SEQUE	NCE DESCRIPTION:	SEQ ID NO:1:		
GGACTCGGAA ATGA	AGGTCCA AGGGTAGC		T GCA GCT TCA TAT a Ala Ala Ser Tyr	
		1	5	. 1100
			GAG AAC TCA AAT	
GIn Leu Leu Lys 10		a Leu Lys Met 5	Glu Asn Ser Asn 20	Leu
			ACA AAA CTG GAA	
arg Gin Giu Let 25	a Glu Asp Asn Se 30	r Asn His Leu	Thr Lys Leu Glu 35	Thr
			CTA CAA GGA AGT	
Glu Ala Ser Asr 40	n Met Lys Glu Va 45	I Leu Lys GIn 50	Leu Gln Gly Ser	55
			GAT TTA TTA GAG	
Glu Asp Glu Ala	a Met Ala Ser Se 60	r Gly Gln Ile 65	Asp Leu Leu Glu 70	Arg
CTT AAA GAG CTT	r aac tta gat ag	C AGT AAT TTC	CCT GGA GTA AAA	CTG 294
Leu Lys Glu Leu 75		r Ser Asn Phe 80	Pro Gly Val Lys 85	Leu
CGG TCA AAA ATO	G TCC CTC CGT TC	T TAT GGA AGC	CGG GAA GGA TCT	GTA 342
Arg Ser Lys Met	Ser Leu Arg Se 9		Arg Glu Gly Ser 100	Val
50	,	-	200	

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 9606 base pairs(B) TYPE: nucleic acid

		GAG Glu							390
		AAT Asn 125							438
		AGG Arg							486
		TGG Trp							534
		CCT Pro							582
		TTG Leu							630
		GGT Gly 205							678
		ATT Ile							726
		TCC Ser							774
		GGC Gly							822
		ATC Ile							870
		GAC Asp 285				Val			918
		Pro			Ser			AAG Lys	966



			GTG Val 315													1014
			TCG Ser													1062
			ATG Met													1110
TTA Leu 360	CAT His	GGC Gly	AAT Asn	GAC Asp	AAA Lys 365	GAC Asp	TCT Ser	GTA Val	TTG Leu	TTG Leu 370	GGA Gly	AAT Asn	TCC Ser	CGG Arg	GGC Gly 375	1158
AGT Ser	AAA Lys	GAG Glu	GCT Ala	CGG Arg 380	GCC Ala	AGG Arg	GCC Ala	AGT Ser	GCA Ala 385	GCA Ala	CTC Leu	CAC His	AAC Asn	ATC Ile 390	ATT Ile	1206
			CCT Pro 395													1254
			GAA Glu													1302
			CAT His													1350
			GAA Glu													1398
CTT Leu	TCA Ser	TTT Phe	GAT Asp	GAA Glu 460	GAG Glu	CAT His	AGA Arg	CAT	GCA Ala 465	ATG Met	AAT Asn	GAA Glu	CTA Leu	GGG Gly 470	GGA Gly	1446
CTA Leu	CAG Gln	GCC Ala	ATT Ile 475	Ala	GAA Glu	TTA Leu	TTG Leu	CAA Gln 480	Val	GAC Asp	TGT Cys	GAA Glu	ATG Met 485	TAT Tyr	GGG Gly	1494
CTT Leu	ACT Thr	AAT Asn 490	Asp	CAC His	TAC Tyr	AGT Ser	ATT Ile 495	Thr	CTA Leu	AGA Arg	CGA Arg	TAT Tyr 500	Ala	GGA Gly	ATG Met	1542
GCT Ala	TTG Leu	ACA Thr	AAC Asn	TTG Leu	ACT Thr	TTI Phe	GGA Gly	GAT Asp	GTA Val	GCC Ala	AAC Asn	AAG Lys	GCT Ala	ACG Thr	CTA Leu	1590



TGC TCT ATG AAA GGC TGC ATG AGA GCA CTT GTG GCC CAA CTA AAA TCT Cys Ser Met Lys Gly Cys Met Arg Ala Leu Val Ala Gln Leu Lys Ser GAA AGT GAA GAC TTA CAG CAG GTT ATT GCA AGT GTT TTG AGG AAT TTG Glu Ser Glu Asp Leu Gln Gln Val Ile Ala Ser Val Leu Arg Asn Leu TCT TGG CGA GCA GAT GTA AAT AGT AAA AAG ACG TTG CGA GAA GTT GGA Ser Trp Arg Ala Asp Val Asn Ser Lys Lys Thr Leu Arg Glu Val Gly AGT GTG AAA GCA TTG ATG GAA TGT GCT TTA GAA GTT AAA AAG GAA TCA Ser Val Lys Ala Leu Met Glu Cys Ala Leu Glu Val Lys Lys Glu Ser ACC CTC AAA AGC GTA TTG AGT GCC TTA TGG AAT TTG TCA GCA CAT TGC Thr Leu Lys Ser Val Leu Ser Ala Leu Trp Asn Leu Ser Ala His Cys ACT GAG AAT AAA GCT GAT ATA TGT GCT GTA GAT GGT GCA CTT GCA TTT Thr Glu Asn Lys Ala Asp Ile Cys Ala Val Asp Gly Ala Leu Ala Phe TTG GTT GGC ACT CTT ACT TAC CGG AGC CAG ACA AAC ACT TTA GCC ATT Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln Thr Asn Thr Leu Ala Ile ATT GAA AGT GGA GGT GGG ATA TTA CGG AAT GTG TCC AGC TTG ATA GCT Ile Glu Ser Gly Gly Gly Ile Leu Arg Asn Val Ser Ser Leu Ile Ala ACA AAT GAG GAC CAC AGG CAA ATC CTA AGA GAG AAC AAC TGT CTA CAA Thr Asn Glu Asp His Arg Gln Ile Leu Arg Glu Asn Asn Cys Leu Gln ACT TTA TTA CAA CAC TTA AAA TCT CAT AGT TTG ACA ATA GTC AGT AAT Thr Leu Leu Gln His Leu Lys Ser His Ser Leu Thr Ile Val Ser Asn GCA TGT GGA ACT TTG TGG AAT CTC TCA GCA AGA AAT CCT AAA GAC CAG Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala Arg Asn Pro Lys Asp Gln GAA GCA TTA TGG GAC ATG GGG GCA GTT AGC ATG CTC AAG AAC CTC ATT Glu Ala Leu Trp Asp Met Gly Ala Val Ser Met Leu Lys Asn Leu Ile

		ATG Met						2214
	_	AGG Arg						2262
		TTG Leu						2310
		GAT Asp 765						2358
		CCC Pro						 2406
		GGT Gly						2454
		AAT Asn						2502
		ACA Thr						2550
		CGT Arg 845				-		2598
		GGC Gly						2646
		GGT Gly					 	2694
		GAA Glu						2742
		ACC Thr						2790

AAT Asn 920	GCA Ala	CTT Leu	AGA Arg	AGA Arg	AGC Ser 925	TCT Ser	GCT Ala	GCC Ala	CAT His	ACA Thr 930	CAT His	TCA Ser	AAC Asn	ACT Thr	TAC Tyr 935	2838
					GAA Glu											2886
					AAG Lys											2934
					TAT Tyr											2982
					GAT Asp											3030
	Pro				GCC Ala 1005	His					Ala					3078
					CTA Leu O					Asn					Tyr	3126
				Leu	AAC Asn				Gln					Asn		3174
			Arg		AAA Lys			Ile					Lys			3222
GAG Glu	CAA Gln 106	Arg	CAA Gln	TCA Ser	AGG Arg	AAT Asn 107	Gln	AGT Ser	ACA Thr	ACT Thr	тат туг 107	Pro	GTT Val	TAT Tyr	ACT Thr	3270
	Ser					His					Pro				CAG Gln 1095	3318
CAG Gln	GAA Glu	TGT Cys	GTT Val	TCT Ser 110	Pro	TAC Tyr	AGG Arg	TCA Ser	CGG Arg 110	Gly	GCC Ala	AAT Asn	GGT Gly	TCA Ser 111	GAA Glu O	3366

ACA AAT CGA GTG Thr Asn Arg Val 1115	Gly Ser Asn	CAT GGA ATT His Gly Ile 1120	AAT CAA AAT Asn Gln Asn	GTA AGC Val Ser 1125	CAG 3414 Gln
TCT TTG TGT CAA Ser Leu Cys Gln 1130	GAA GAT GAC Glu Asp Asp	TAT GAA GAT Tyr Glu Asr 1135	G GAT AAG CCT Asp Lys Pro 114	Thr Asn	TAT 3462 Tyr
AGT GAA CGT TAC Ser Glu Arg Tyr 1145	TCT GAA GAA Ser Glu Glu 1150	Glu Gln His	GAA GAA GAA Glu Glu Glu 1155	GAG AGA Glu Arg	CCA 3510 Pro
ACA AAT TAT AGC Thr Asn Tyr Ser 1160	ATA AAA TAT Ile Lys Tyr 1165	AAT GAA GAO Asn Glu Glu	G AAA CGT CAT 1 Lys Arg His 1170	GTG GAT Val Asp	CAG 3558 Gln 1175
CCT ATT GAT TAT Pro Ile Asp Tyr	AGT TTA AAA Ser Leu Lys 1180	TAT GCC ACA	Asp Ile Pro	TCA TCA Ser Ser 1190	Gln
AAA CAG TCA TTT Lys Gln Ser Phe 1199	Ser Phe Ser	AAG AGT TCA Lys Ser Ser 1200	A TCT GGA CAA r Ser Gly Gln	AGC AGT Ser Ser 1205	AAA 3654 Lys
ACC GAA CAT ATG Thr Glu His Met 1210	TCT TCA AGC Ser Ser Ser	AGT GAG AA' Ser Glu Ası 1215	T ACG TCC ACA n Thr Ser Thr 122	Pro Ser	TCT 3702 Ser
AAT GCC AAG AGG Asn Ala Lys Arg 1225	CAG AAT CAG Gln Asn Gln 123	Leu His Pro	A AGT TCT GCA o Ser Ser Ala 1235	CAG AGT Gln Ser	AGA 3750 Arg
AGT GGT CAG CCT Ser Gly Gln Pro 1240	CAA AAG GCT Gln Lys Ala 1245	GCC ACT TG	C AAA GTT TCT s Lys Val Ser 1250	TCT ATT	AAC 3798 Asn 1255
CAA GAA ACA ATA Gln Glu Thr Ile	CAG ACT TAT Gln Thr Tyr 1260	TGT GTA GA Cys Val Gl 12	u Asp Thr Pro	A ATA TGT o Ile Cys 127	Phe
TCA AGA TGT AGT Ser Arg Cys Ser 127	Ser Leu Ser	TCT TTG TC Ser Leu Se 1280	A TCA GCT GAA r Ser Ala Glu	A GAT GAA 1 Asp Glu 1285	ATA 3894 Ile
GGA TGT AAT CAG Gly Cys Asn Gln 1290	ACG ACA CAG	GAA GCA GA Glu Ala As 1295	T TCT GCT AA p Ser Ala Ass 13	n Thr Leu	CAA 3942 Gln
ATA GCA GAA ATA Ile Ala Glu Ile 1305	AAA GGA AAG Lys Gly Lys 131	: Ile Gly Th	T AGG TCA GC ir Arg Ser Al 1315	r GAA GAT a Glu Asp	CCT 3990 Pro

GTG AGC GAA Val Ser Glu 1320	GTT CCA GCA G Val Pro Ala V 1325	TG TCA CAG al Ser Gln	CAC CCT AGA His Pro Arg 1330	ACC AAA TCC Thr Lys Ser	AGC 4038 Ser 1335
AGA CTG CAG Arg Leu Gln	GGT TCT AGT T Gly Ser Ser L 1340	TA TCT TCA eu Ser Ser	GAA TCA GCC Glu Ser Ala 1345	AGG CAC AAA Arg His Lys 1350	Ala
GTT GAA TTT Val Glu Phe	CCT TCA GGA G Pro Ser Gly A 1355	CG AAA TCT Ala Lys Ser 1360	Pro Ser Lys	AGT GGT GCT Ser Gly Ala 1365	CAG 4134 Gln
ACA CCC AAA Thr Pro Lys 1370	AGT CCA CCT G Ser Pro Pro G O	GAA CAC TAT Glu His Tyr 1375	GTT CAG GAG Val Gln Glu	ACC CCA CTC Thr Pro Leu 1380	ATG 4182 Met
TTT AGC AGA Phe Ser Arg 1385	TGT ACT TCT C Cys Thr Ser V	GTC AGT TCA Val Ser Ser 1390	CTT GAT AGT Leu Asp Ser 139	Phe Glu Ser	CGT 4230 Arg
TCG ATT GCC Ser Ile Ala 1400	AGC TCC GTT (Ser Ser Val (1405	CAG AGT GAA Gln Ser Glu	CCA TGC AGT Pro Cys Ser 1410	GGA ATG GTA Gly Met Val	AGT 4278 Ser 1415
GGC ATT ATA Gly Ile Ile	AGC CCC AGT (Ser Pro Ser A 1420	GAT CTT CCA Asp Leu Pro	GAT AGC CCT Asp Ser Pro 1425	GGA CAA ACC Gly Gln Thr 143	Met
CCA CCA AGC Pro Pro Ser	AGA AGT AAA A Arg Ser Lys 1 1435	ACA CCT CCA Thr Pro Pro 144	Pro Pro Pro	CAA ACA GCT Gln Thr Ala 1445	CAA 4374 Gln
ACC AAG CGA Thr Lys Arg 145	GAA GTA CCT A Glu Val Pro 1	AAA AAT AAA Lys Asn Lys 1455	GCA CCT ACT Ala Pro Thr	GCT GAA AAG Ala Glu Lys 1460	AGA 4422 Arg
GAG AGT GGA Glu Ser Gly 1465	CCT AAG CAA	GCT GCA GTA Ala Ala Val 1470	AAT GCT GCA Asn Ala Ala 147	ı Val Gln Arg	GTC 4470 Val
CAG GTT CTT Gln Val Leu 1480	CCA GAT GCT Pro Asp Ala 1485	Asp Thr Leu	TTA CAT TTT Leu His Pho 1490	GCC ACA GAA Ala Thr Glu	A AGT 4518 1 Ser 1495
ACT CCA GAT Thr Pro Asp	GGA TTT TCT GGly Phe Ser 1500	TGT TCA TCC Cys Ser Ser	AGC CTG AGT Ser Leu Ser 1505	r GCT CTG AGC r Ala Leu Sei 151	Leu





GAT GAG CCA TTT ATA CAG AAA GAT GTG GAA TTA AGA ATA ATG CCT CCA Asp Glu Pro Phe Ile Gln Lys Asp Val Glu Leu Arg Ile Met Pro Pro 1515 1520 1525	4614
GTT CAG GAA AAT GAC AAT GGG AAT GAA ACA GAA TCA GAG CAG CCT AAA Val Gln Glu Asn Asp Asn Gly Asn Glu Thr Glu Ser Glu Gln Pro Lys 1530 1535 1540	4662
GAA TCA AAT GAA AAC CAA GAG AAA GAG GCA GAA AAA ACT ATT GAT TCT Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala Glu Lys Thr Ile Asp Ser 1545 1550 1555	4710
GAA AAG GAC CTA TTA GAT GAT TCA GAT GAT GAT GAT ATT GAA ATA CTA Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp Asp Ile Glu Ile Leu 1560 1565 1570 1575	4758
GAA GAA TGT ATT ATT TCT GCC ATG CCA ACA AAG TCA TCA CGT AAA GGC Glu Glu Cys Ile Ile Ser Ala Met Pro Thr Lys Ser Ser Arg Lys Gly 1580	4806
AAA AAG CCA GCC CAG ACT GCT TCA AAA TTA CCT CCA CCT GTG GCA AGG Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu Pro Pro Pro Val Ala Arg 1595 1600 1605	4854
AAA CCA AGT CAG CTG CCT GTG TAC AAA CTT CTA CCA TCA CAA AAC AGG Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu Leu Pro Ser Gln Asn Arg 1610 1615 1620	4902
TTG CAA CCC CAA AAG CAT GTT AGT TTT ACA CCG GGG GAT GAT ATG CCA Leu Gln Pro Gln Lys His Val Ser Phe Thr Pro Gly Asp Asp Met Pro 1625 1630 1635	4950
CGG GTG TAT TGT GTT GAA GGG ACA CCT ATA AAC TTT TCC ACA GCT ACA Arg Val Tyr Cys Val Glu Gly Thr Pro Ile Asn Phe Ser Thr Ala Thr 1640 1645 1650 1655	4998
TCT CTA AGT GAT CTA ACA ATC GAA TCC CCT CCA AAT GAG TTA GCT GCT Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro Pro Asn Glu Leu Ala Ala 1660 1665 1670	5046
GGA GAA GGA GTT AGA GGA GGA GCA CAG TCA GGT GAA TTT GAA AAA CGA Gly Glu Gly Val Arg Gly Gly Ala Gln Ser Gly Glu Phe Glu Lys Arg 1675 1680 1685	5094
GAT ACC ATT CCT ACA GAA GGC AGA AGT ACA GAT GAG GCT CAA GGA GGA Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr Asp Glu Ala Gln Gly Gly 1690 1695 1700	5142
AAA ACC TCA TCT GTA ACC ATA CCT GAA TTG GAT GAC AAT AAA GCA GAG Lys Thr Ser Ser Val Thr Ile Pro Glu Leu Asp Asp Asn Lys Ala Glu 1705 1710 1715	5190



GAA GGT GAT Glu Gly Asp 1720	ATT CTT GCA Ile Leu Ala 1725	Glu Cys Ile	AAT TCT GCT Asn Ser Ala 1730	ATG CCC AAA Met Pro Lys	GGG 5238 Gly 1735
AAA AGT CAC Lys Ser His	AAG CCT TTC Lys Pro Phe 1740	CGT GTG AAAAArg Val Lys	AAG ATA ATG Lys Ile Met 1745	G GAC CAG GTC Asp Gln Val 1750	Gin
CAA GCA TCT Gln Ala Ser	GCG TCG TCT Ala Ser Ser 1755	TCT GCA CCC Ser Ala Pro 176	Asn Lys Asn	C CAG TTA GAT I Gln Leu Asp 1765	GGT 5334 Gly
AAG AAA AAG Lys Lys Lys 1770	Lys Pro Thr	TCA CCA GTA Ser Pro Val 1775	AAAA CCT ATA Lys Pro Ile	A CCA CAA AAT e Pro Gln Asn 1780	ACT 5382 Thr
GAA TAT AGG Glu Tyr Arg 1785	ACA CGT GTA Thr Arg Val	AGA AAA AA' Arg Lys Asi 1790	GCA GAC TCA Ala Asp Ser 179	A AAA AAT AAT r Lys Asn Asn 95	TTA 5430 Leu
AAT GCT GAG Asn Ala Glu 1800	AGA GTT TTC Arg Val Phe 180	Ser Asp As	C AAA GAT TCA n Lys Asp Sei 1810	A AAG AAA CAG r Lys Lys Gln	AAT 5478 Asn 1815
TTG AAA AAT Leu Lys Asn	AAT TCC AAG Asn Ser Lys 1820	GAC TTC AA Asp Phe As	r GAT AAG CTO n Asp Lys Leo 1825	C CCA AAT AAT u Pro Asn Asn 183	. GIU
GAT AGA GTC Asp Arg Val	AGA GGA AGT Arg Gly Ser 1835	TTT GCT TT Phe Ala Ph 18	e Asp Ser Pr	T CAT CAT TAC o His His Tyr 1845	: ACG 5574 : Thr
CCT ATT GAA Pro Ile Glu 185	Gly Thr Pro	TAC TGT TTO TYR Cys Ph 1855	T TCA CGA AA e Ser Arg As	T GAT TCT TTO n Asp Ser Let 1860	G AGT 5622 1 Ser
TCT CTA GAT Ser Leu Asp 1865	TTT GAT GAT Phe Asp Asp	GAT GAT GT Asp Asp Va 1870	l Asp Leu Se	C AGG GAA AAC er Arg Glu Lys 375	G GCT 5670 S Ala
GAA TTA AGA Glu Leu Arg 1880	A AAG GCA AAA J Lys Ala Lys 18	s Glu Asn Ly	G GAA TCA GA s Glu Ser Gl 1890	AG GCT AAA GT Lu Ala Lys Va	F ACC 5718 1 Thr 1895
AGC CAC ACA	A GAA CTA AC Glu Leu Th 1900	C TCC AAC CA r Ser Asn G	AA CAA TCA GO In Gln Ser Al 1905	CT AAT AAG AC. la Asn Lys Th 19	r GIN



GCT ATT GCA AAAA Ala Ile Ala Ly		Ile Asn				Ile		5814
CAG AAA CAA TO Gln Lys Gln Se 1930			Ser Ser					5862
GGG GCA GCA AG Gly Ala Ala Th 1945	nr Asp Glu				Ile Glu		-	5910
CCA GTT TGC TT Pro Val Cys Ph 1960		Asn Ser				Asp		5958
GAC CAA GAA AA Asp Gln Glu As				Pro Ile			Glu	6006
CCC CCT GAC TO Pro Pro Asp Se		Glu Pro				Gly		6054
GCT CCT AAA TO Ala Pro Lys So 2010			Asp Thr					6102
AAC AGT TCT CT Asn Ser Ser Le 2025	eu Ser Ser				Asp Asp			6150
CAG GAA TGT AGGIN Glu Cys II		Ala Met						6198
CTC AAG GGT G				Arg Asn			Ile	6246
TTA GGT GAA G Leu Gly Glu A						Pro		6294
TCA GAA CAT G Ser Glu His G 2090			Ser Glu					6342
ATT CAG GAA G Ile Gln Glu G 2105	ly Ala Asn				His Gln			6390

GCT GCT GCA TGT TTA TCT AGA CAA GCT TCG TCT GAT TCA GAT TCC ATC Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser Ser Asp Ser Asp Ser Ile 2120 2125 2130 2135	6438
CTT TCC CTG AAA TCA GGA ATC TCT CTG GGA TCA CCA TTT CAT CTT ACA Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly Ser Pro Phe His Leu Thr 2140 2145 2150	6486
CCT GAT CAA GAA GAA AAA CCC TTT ACA AGT AAT AAA GGC CCA CGA ATT Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser Asn Lys Gly Pro Arg Ile 2155 2160 2165	6534
CTA AAA CCA GGG GAG AAA AGT ACA TTG GAA ACT AAA AAG ATA GAA TCT Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu Thr Lys Lys Ile Glu Ser 2170 2175 2180	6582
GAA AGT AAA GGA ATC AAA GGA GGA AAA AAA GTT TAT AAA AGT TTG ATT Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys Val Tyr Lys Ser Leu Ile 2185 2190 2195	6630
ACT GGA AAA GTT CGA TCT AAT TCA GAA ATT TCA GGC CAA ATG AAA CAG Thr Gly Lys Val Arg Ser Asn Ser Glu Ile Ser Gly Gln Met Lys Gln 2200 2205 2210 2215	6678
CCC CTT CAA GCA AAC ATG CCT TCA ATC TCT CGA GGC AGG ACA ATG ATT Pro Leu Gln Ala Asn Met Pro Ser Ile Ser Arg Gly Arg Thr Met Ile 2220 2225 2230	6726
CAT ATT CCA GGA GTT CGA AAT AGC TCC TCA AGT ACA AGT CCT GTT TCT His Ile Pro Gly Val Arg Asn Ser Ser Ser Ser Thr Ser Pro Val Ser 2235 2240 2245	6774
AAA AAA GGC CCA CCC CTT AAG ACT CCA GCC TCC AAA AGC CCT AGT GAA Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala Ser Lys Ser Pro Ser Glu 2250 2255 2260	6822
GGT CAA ACA GCC ACC ACT TCT CCT AGA GGA GCC AAG CCA TCT GTG AAA Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly Ala Lys Pro Ser Val Lys 2265 2270 2275	6870
TCA GAA TTA AGC CCT GTT GCC AGG CAG ACA TCC CAA ATA GGT GGG TCA Ser Glu Leu Ser Pro Val Ala Arg Gln Thr Ser Gln Ile Gly Gly Ser 2280 2285 2290 2295	6918
AGT AAA GCA CCT TCT AGA TCA GGA TCT AGA GAT TCG ACC CCT TCA AGA Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg Asp Ser Thr Pro Ser Arg 2300 2305 2310	6966



CCT GCC CAG CAA CCA TTA AGT AGA CCT ATA CAG TCT CCT GGC CGA AAC Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile Gln Ser Pro Gly Arg Asn 2315 2320 2325	7014
TCA ATT TCC CCT GGT AGA AAT GGA ATA AGT CCT CCT AAC AAA TTA TCT Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser Pro Pro Asn Lys Leu Ser 2330 2335 2340	7062
CAA CTT CCA AGG ACA TCA TCC CCT AGT ACT GCT TCA ACT AAG TCC TCA Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr Ala Ser Thr Lys Ser Ser 2345 2350 2355	7110
GGT TCT GGA AAA ATG TCA TAT ACA TCT CCA GGT AGA CAG ATG AGC CAA Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro Gly Arg Gln Met Ser Gln 2360 2375	7158
CAG AAC CTT ACC AAA CAA ACA GGT TTA TCC AAG AAT GCC AGT AGT ATT Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser Lys Asn Ala Ser Ser Ile 2380 2385 2390	7206
CCA AGA AGT GAG TCT GCC TCC AAA GGA CTA AAT CAG ATG AAT AAT GGT Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu Asn Gln Met Asn Asn Gly 2395 2400 2405	7254
AAT GGA GCC AAT AAA AAG GTA GAA CTT TCT AGA ATG TCT TCA ACT AAA Asn Gly Ala Asn Lys Lys Val Glu Leu Ser Arg Met Ser Ser Thr Lys 2410 2415 2420	7302
TCA AGT GGA AGT GAA TCT GAT AGA TCA GAA AGA CCT GTA TTA GTA CGC Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu Arg Pro Val Leu Val Arg 2425 2430 2435	7350
CAG TCA ACT TTC ATC AAA GAA GCT CCA AGC CCA ACC TTA AGA AGA AAA Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser Pro Thr Leu Arg Arg Lys 2440 2445 2450 2450	7398
TTG GAG GAA TCT GCT TCA TTT GAA TCT CTT TCT CCA TCA TCT AGA CCA Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu Ser Pro Ser Ser Arg Pro 2460 2465 2470	7446
GCT TCT CCC ACT AGG TCC CAG GCA CAA ACT CCA GTT TTA AGT CCT TCC Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr Pro Val Leu Ser Pro Ser 2475 2480 2485	7494
CTT CCT GAT ATG TCT CTA TCC ACA CAT TCG TCT GTT CAG GCT GGA Leu Pro Asp Met Ser Leu Ser Thr His Ser Ser Val Gln Ala Gly Gly 2490 2495 2500	7542
TGG CGA AAA CTC CCA CCT AAT CTC AGT CCC ACT ATA GAG TAT AAT GAT Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro Thr Ile Glu Tyr Asn Asp 2505 2510 2515	7590

GGA AGA CCA Gly Arg Pro 2520	GCA AAG CGC Ala Lys Arg 252	g His Asp	Ile Ala A	GG TCT CAT rg Ser His 530	Ser Glu Se	GT 7638 er 535
CCT TCT AGA Pro Ser Arg	CTT CCA ATC Leu Pro Ile 2540	C AAT AGG	TCA GGA A Ser Gly I 2545	CC TGG AAA	CGT GAG CA Arg Glu Hi 2550	AC 7686 is
AGC AAA CAT Ser Lys His	TCA TCA TCC Ser Ser Ser 2555	r Leu Pro	CGA GTA A Arg Val S 2560	Ser Thr Trp	AGA AGA AG Arg Arg Tl 2565	CT 7734 hr
GGA AGT TCA Gly Ser Ser 257	TCT TCA AT Ser Ser Il	r CTT TCT e Leu Ser 2575	Ala Ser S	TCA GAA TCC Ser Glu Ser 2580	Ser Glu L	AA 7782 ys
GCA AAA AGT Ala Lys Ser 2585	GAG GAT GA Glu Asp Gl	A AAA CAT u Lys His 2590	GTG AAC T Val Asn S	CT ATT TCA Ser Ile Ser 2595	GGA ACC A Gly Thr L	AA 7830 ys
CAA AGT AAA Gln Ser Lys 2600	GAA AAC CA Glu Asn Gl 26	n Val Ser	Ala Lys (GGA ACA TGG Gly Thr Trp 2610	Arg Lys I	TA 7878 le 615
AAA GAA AAT Lys Glu Asr	GAA TTT TC Glu Phe Se 2620	T CCC ACA r Pro Thr	AAT AGT A Asn Ser 7 2625	ACT TCT CAG Thr Ser Gln	ACC GTT T Thr Val S 2630	CC 7926 er
TCA GGT GCT Ser Gly Ala	T ACA AAT GG a Thr Asn Gl 2635	T GCT GAA y Ala Glu	TCA AAG A Ser Lys ' 2640	ACT CTA ATT Thr Leu Ile	TAT CAA A Tyr Gln M 2645	TG 7974 let
GCA CCT GCT Ala Pro Ala 26	r GTT TCT AF a Val Ser Ly 50	A ACA GAG rs Thr Glu 2659	Asp Val	TGG GTG AGA Trp Val Arg 266	Ile Glu A	SAC 8022 Asp
TGT CCC AT Cys Pro Il 2665	r AAC AAT CC e Asn Asn Pi	T AGA TCT O Arg Ser 2670	GGA AGA Gly Arg	TCT CCC ACA Ser Pro Thr 2675	GGT AAT A	ACT 8070 Fhr
CCC CCG GT Pro Pro Va 2680	G ATT GAC AG 1 Ile Asp Se 20	GT GTT TCA er Val Ser 585	GAA AAG Glu Lys	GCA AAT CCA Ala Asn Pro 2690	Asn Ile I	AAA 8118 Lys 2695
GAT TCA AA Asp Ser Ly	A GAT AAT CA s Asp Asn G 2700	AG GCA AAA ln Ala Lys	CAA AAT Gln Asn 2705	Val Gly Asn	GGC AGT (Gly Ser V 2710	GTT 8166 Val
CCC ATG CG Pro Met Ar	T ACC GTG G g Thr Val G 2715	GT TTG GAA ly Leu Glu	AAT CGC Asn Arg 2720	CTG ACC TCC Leu Thr Ser	TTT ATT (Phe Ile (2725	CAG 8214 Gln



GTG GAT GCC CCT GAC CAA AAA GGA ACT GAG ATA AAA CCA GGA CAA AAT Val Asp Ala Pro Asp Gln Lys Gly Thr Glu Ile Lys Pro Gly Gln Asn 2730 2740	8262
AAT CCT GTC CCT GTA TCA GAG ACT AAT GAA AGT CCT ATA GTG GAA CGT Asn Pro Val Pro Val Ser Glu Thr Asn Glu Ser Pro Ile Val Glu Arg 2745 2750 2755	8310
ACC CCA TTC AGT TCT AGC AGC TCA AGC AAA CAC AGT TCA CCT AGT GGG Thr Pro Phe Ser Ser Ser Ser Ser Lys His Ser Ser Pro Ser Gly 2760 2765 2770 2775	8358
ACT GTT GCT GCC AGA GTG ACT CCT TTT AAT TAC AAC CCA AGC CCT AGG Thr Val Ala Ala Arg Val Thr Pro Phe Asn Tyr Asn Pro Ser Pro Arg 2780 2785 2790	8406
AAA AGC AGC GCA GAT AGC ACT TCA GCT CGG CCA TCT CAG ATC CCA ACT Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg Pro Ser Gln Ile Pro Thr 2795 2800 2805	8454
CCA GTG AAT AAC AAC ACA AAG AAG CGA GAT TCC AAA ACT GAC AGC ACA Pro Val Asn Asn Asn Thr Lys Lys Arg Asp Ser Lys Thr Asp Ser Thr 2810 2815 2820	8502
GAA TCC AGT GGA ACC CAA AGT CCT AAG CGC CAT TCT GGG TCT TAC CTT Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg His Ser Gly Ser Tyr Leu 2825 2830 2835	8550
GTG ACA TCT GTT TAAAAGAGAG GAAGAATGAA ACTAAGAAAA TTCTATGTTA Val Thr Ser Val 2840	8602
ATTACAACTG CTATATAGAC ATTTTGTTTC AAATGAAACT TTAAAAGACT GAAAAATTTT	8662
GTAAATAGGT TTGATTCTTG TTAGAGGGTT TTTGTTCTGG AAGCCATATT TGATAGTATA	8722
CTTTGTCTTC ACTGGTCTTA TTTTGGGAGG CACTCTTGAT GGTTAGGAAA AAATAGAAAG	8782
CCAAGTATGT TTGTACAGTA TGTTTTACAT GTATTTAAAG TAGCATCCCA TCCCAACTTC	8842
CTTAATTATT GCTTGTCTAA AATAATGAAC ACTACAGATA GGAAATATGA TATATTGCTG	8902
TTATCAATCA TTTCTAGATT ATAAACTGAC TAAACTTACA TCAGGGGAAA ATTGGTATTT	8962
ATGCAAAAA AAAATGTTTT TGTCCTTGTG AGTCCATCTA ACATCATAAT TAATCATGTG	9022
GCTGTGAAAT TCACAGTAAT ATGGTTCCCG ATGAACAAGT TTACCCAGCC TGCTTTGCTT	9082
ACTGCATGAA TGAAACTGAT GGTTCAATTT CAGAAGTAAT GATTAACAGT TATGTGGTCA	9142

_	ATGT	GC A	TAGA	GATA	G CI	'ACAG	TGTA	ATA	rtta.	'ACA	СТАТ	TTTG	TG (CTCCA	AACA
AACA	AAAA	TC T	GTGT	AACT	G TA	AAAC	ATTG	AAT	'GAAA	CTA	TTTT	'ACCT	'GA	ACTAG	ATTT
ATCT	'GAAA	GT A	.GGTA	GAAT	TT T	TGCT	ATGC	TGT	l'TAA'	TGT	TGTA	TTAT	CT (GGTAT	'TTGA(
GTGA	GATG	GC T	'GCTC	TTTA	т та	ATGA	GACA	TGA	ATTO	TGT	CTCA	ACAG	AA A	ACTAA	ATGA?
CATT	TCAC	L AA	TAAA'	TATT	G CI	'GTAT	GTAA	ACI	GTTA	CTG	LAAA	'TGGT	'TA'	ГТGТТ	TGAA
GGTT	TGTT	TC A	CATT	TGTA	T T	ATT <i>P</i>	ATTG	TTI	'AAAA'	TGC	CTCT	TTTA	AA .	AGCTI	TATAT
AATT	TTTT	'CT T	'CAGC	TTCT	'A TO	CATT	'AAGA	GTA	raaa.	TCC	TCTT	ACTG	TA Z	АТААА	AACAT
TGAA	GAAG	AC T	'GT'TG	CCAC	T TA	ACCA	ATTCC	ATC	CGTT	'GGC	ACTI	1			
(2)	INFO	RMAT	NOI	FOR	SEQ	ID N	10:2:								
	(i) S					ERIST 13 am			ls					
			(B)	TYF	E: 6	mino	aci	.d							
			(D)	TOP	OLOC	Y:]	linea	ır							
	(i	.i) M	OLEC	ULE	TYPI	E: pr	rotei	n							
		·				_	rotei TION:) ID	NO:2	2:				
Met 1	(3	xi) S	SEQUE	NCE	DESC	RIP	: NOI	SEÇ				Val	Glu	Ala 15	Leu
1	(2 Ala	ci) S Ala	SEQUE Ala	Ser 5	DES(CRIPT Asp	FION: Gln	SEÇ Leu	Leu 10	Lys	Gln			15 Ser	
1 Lys	() Ala Met	xi) S Ala Glu	EEQUE Ala Asn 20	Ser 5 Ser	DESC Tyr Asn	CRIPT Asp Leu	FION: Gln Arg	SEÇ Leu Gln 25	Leu 10 Glu	Lys Leu	Gln Glu	Asp	Asn 30	15 Ser	Asn
1 Lys His	() Ala Met Leu	Ala Glu Thr 35	Ala Asn 20 Lys	Ser 5 Ser Leu	DESC Tyr Asn Glu	Asp Leu	Gln Arg Glu 40	SEQ Leu Gln 25 Ala	Leu 10 Glu Ser	Lys Leu Asn	Gln Glu Met	Asp Lys 45	Asn 30 Glu	15 Ser	Asn Leu
1 Lys His Lys	(2 Ala Met Leu Gln 50	Ala Glu Thr 35 Leu	Ala Asn 20 Lys Gln	Ser 5 Ser Leu Gly	DESC Tyr Asn Glu Ser	Asp Leu Thr	Gln Arg Glu 40 Glu	SEQ Leu Gln 25 Ala Asp	Leu 10 Glu Ser	Lys Leu Asn Ala	Gln Glu Met Met 60	Asp Lys 45 Ala	Asn 30 Glu Ser	15 Ser Val	Asn Leu Gly
Lys His Lys Gln 65	(xAla Met Leu Gln 50	Ala Glu Thr 35 Leu Asp	Ala Asn 20 Lys Gln Leu	Ser 5 Ser Leu Gly	DESC Tyr Asn Glu Ser Glu 70	Asp Leu Thr Ile 55	Glu Glu Glu Leu	SEQ Leu Gln 25 Ala Asp	Leu 10 Glu Ser Glu	Lys Leu Asn Ala Leu 75	Gln Glu Met Met 60 Asn	Asp Lys 45 Ala Leu	Asn 30 Glu Ser	15 Ser Val	Asn Leu Gly Ser 80

Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg 115 120 125

Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu Pro Leu Thr Glu Asn Phe Ser Leu Gln Thr Asp Leu Thr Arg Arg Gln Leu Glu Tyr Glu Ala Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln Asp Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp Ala Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala Thr Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr Ser His Leu Gly Thr Lys Val Glu Met Val Tyr Ser Leu Leu Ser Met Leu Gly Thr His Asp Lys Asp Asp Met Ser Arg Thr Leu Leu Ala Met Ser Ser Ser Gln Asp Ser Cys Ile Ser Met Arg Gln Ser Gly Cys Leu Pro Leu Leu Ile Gln Leu Leu His Gly Asn Asp Lys Asp Ser Val Leu Leu Gly Asn Ser Arg Gly Ser Lys Glu Ala Arg Ala Arg Ala Ser

Ala Ala Leu His Asn Ile Ile His Ser Gln Pro Asp Asp Lys Arg Gly

Arg	Arg	Glu	Ile	Arg 405	Val	Leu	His	Leu	Leu 410	Glu	Gln	Ile	Arg	Ala 415	Tyr
Cys	Glu	Thr	Cys 420	Trp	Glu	Trp	Gln	Glu 425	Ala	His	Glu	Pro	Gly 430	Met	Asp
Gln	Asp	Lys 435	Asn	Pro	Met	Pro	Ala 440	Pro	Val	Glu	His	Gln 445	Ile	Cys	Pro
Ala	Val 450	Cys	Val	Leu	Met	Lys 455	Leu	Ser	Phe	Asp	Glu 460	Glu	His	Arg	His
Ala 465	Met	Asn	Glu	Leu	Gly 470	Gly	Leu	Gln	Ala	Ile 475	Ala	Glu	Leu	Leu	Gln 480
Val	Asp	Cys	Glu	Met 485	Tyr	Gly	Leu	Thr	Asn 490	Asp	His	Tyr	Ser	Ile 495	Thr
Leu	Arg	Arg	Tyr 500	Ala	Gly	Met	Ala	Leu 505	Thr	Asn	Leu	Thr	Phe 510	Gly	Asp
Val	Ala	Asn 515	Lys	Ala	Thr	Leu	Cys 520	Ser	Met	Lys	Gly	Cys 525	Met	Arg	Ala
Leu	Val 530	Ala	Gln	Leu	Lys	Ser 535	Glu	Ser	Glu	Asp	Leu 540	Gln	Gln	Val	Ile
Ala 545	Ser	Val	Leu	Arg	Asn 550	Leu	Ser	Trp	Arg	Ala 555	Asp	Val	Asn	Ser	Lys 560
Lys	Thr	Leu	Arg	Glu 565	Val	Gly	Ser	Val	Lys 570	Ala	Leu	Met	Glu	Cys 575	Ala
Leu	Glu	Val	Lys 580	Lys	Glu	Ser	Thr	Leu 585	Lys	Ser	Val	Leu	Ser 590	Ala	Leu
Trp	Asn	Leu 595		Ala	His	Cys	Thr 600	Glu	Asn	Lys	Ala	Asp 605	Ile	Cys	Ala
Val	Asp 610	Gly	Ala	Leu	Ala	Phe 615		Val	Gly	Thr	Leu 620	Thr	Tyr	Arg	Ser
Gln 625	Thr	Asn	Thr	Leu	Ala 630	Ile	Ile	Glu	Ser	Gly 635		Gly	Ile	Leu	Arg 640
Asn	Val	Ser	Ser	Leu 645	Ile	Ala	Thr	Asn	Glu 650		His	Arg	Gln	Ile 655	Leu
Arg	Glu	Asn	Asn 660		Leu	Gln	Thr	Leu 665		Gln	His	Leu	Lys 670		His

Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn

Arg 945	Thr	Cys	Ser	Met	Pro 950	Tyr	Ala	Lys	Leu	Glu 955	Tyr	Lys	Arg	Ser	Ser 960
Asn	Asp	Ser	Leu	Asn 965	Ser	Val	Ser	Ser	Asn 970	Asp	Gly	Tyr	Gly	Lys 975	Arg
Gly	Gln	Met	Lys 980	Pro	Ser	Ile	Glu	Ser 985	Tyr	Ser	Glu	Asp	Asp 990	Glu	Ser
Lys	Phe	Cys 995	Ser	Tyr	Gly	Gln	Tyr 1000		Ala	Asp	Leu	Ala 100		Lys	Ile
His	Ser 1010		Asn	His	Met	Asp 101		Asn	Asp	Gly	Glu 1020		Asp	Thr	Pro
Ile 1025		Tyr	Ser	Leu	Lys 1030		Ser	Asp	Glu	Gln 1035		Asn	Ser	Gly	Arg 1040
Gln	Ser	Pro	Ser	Gln 1045		Glu	Arg	Trp	Ala 1050		Pro	Lys	His	Ile 1055	
Glu	Asp	Glu	Ile 1060	_	Gln	Ser	Glu	Gln 1065	_	Gln	Ser	Arg	Asn 1070		Ser
Thr	Thr	Tyr 1075		Val	Tyr	Thr	Glu 1080		Thr	Asp	Asp	Lys 1085		Leu	Lys
Phe	Gln 1090		His	Phe	Gly	Gln 1095		Glu	Cys	Val	Ser 110		Tyr	Arg	Ser
Arg 1105		Ala	Asn	Gly	Ser 1110		Thr	Asn	Arg	Val 1115		Ser	Asn	His	Gly 1120
Ile	Asn	Gln	Asn	Val 112		Gln	Ser	Leu	Cys 1130		Glu	Asp	Asp	Tyr 1135	
Asp	Asp	Lys	Pro 1140		Asn	Tyr			_	Tyr		Glu	Glu 1150		Gln
His	Glu	Glu 115		Glu	Arg	Pro	Thr 1160		Tyr	Ser	Ile	Lys 116		Asn	Glu
Glu	Lys 1170	_	His	Val	Asp	Gln 1175		Ile	Asp	Tyr	Ser 118		Lys	Tyr	Ala
Thr 1185		Ile	Pro	Ser	Ser 1190		Lys	Gln	Ser	Phe 119		Phe	Ser	Lys	Ser 1200
Ser	Ser	Gly	Gln	Ser 120		Lys	Thr	Glu	His 1210		Ser	Ser	Ser	Ser 121	

Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Gly Lys Ile Gly Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu Ser Ala Arg His Lys Ala Val Glu Phe Pro Ser Gly Ala Lys Ser Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val

Asn Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu

Leu	His 1490		Ala	Thr	Glu	Ser 1495		Pro	Asp	Gly	Phe 1500	Ser	Cys	Ser	Ser
Ser 1505		Ser	Ala	Leu	Ser 1510		Asp	Glu	Pro	Phe 1515	Ile	Gln	Lys	Asp	Val 1520
Glu	Leu	Arg	Ile	Met 1525		Pro	Val	Gln	Glu 1530	Asn)	Asp	Asn	Gly	Asn 1535	Glu
Thr	Glu	Ser	Glu 1540		Pro	Lys	Glu	Ser 1545	Asn	Glu	Asn	Gln	Glu 1550	Lys	Glu
Ala	Glu	Lys 155		Ile	Asp	Ser	Glu 1560	Lys	Asp	Leu	Leu	Asp 156	Asp 5	Ser	Asp
Asp	Asp 1570		Ile	Glu	Ile	Leu 1575		Glu	Cys	Ile	Ile 158	Ser O	Ala	Met	Pro
Thr 158		Ser	Ser	Arg	Lys 159	Gly O	Lys	Lys	Pro	Ala 159	Gln 5	Thr	Ala	Ser	Lys 1600
Leu	Pro	Pro	Pro	Val 160		Arg	Lys	Pro	Ser 161	Gln 0	Leu	Pro	Val	Tyr 161	Lys
Leu	Leu	Pro	Ser 162		Asn	Arg	Leu	Gln 162	Pro 5	Gln	Lys	His	Val 163	Ser)	Phe
Thr	Pro	Gly 163		Asp	Met	Pro	Arg 164	Val 0	Tyr	Cys	Val	Glu 164	Gly 5	Thr	Pro
Ile	Asn 165		Ser	Thr	Ala	Thr 165		Leu	Ser	Asp	Leu 166	Thr 0	Ile	Glu	Ser
Pro		Asn	Glu	ı Leu	Ala 167		Gly	Glu	Gly	Val 167	Arg	r Gly	gly	Ala	Gln 1680
Ser	Gly	Glu	ı Phe	Glu 168		Arg	Asp	Thr	11e	e Pro	Thr	: Glu	ı Gly	Arg 169	Ser 5
Thr	Asp	Glu	a Ala 170		ı Gly	gly	· Lys	Thr 170	Sei Sei	s Sei	. Val	Thi	171	Pro 0	Glu
Lev	ı Asp	Asp 171		n Lys	s Ala	a Glu	Glu 172		/ Ası	o Ile	e Lei	1 Ala 172	a Glu 25	. Cys	Ile
Ası	n Ser 173		a Me	t Pro	Ly:	s Gly 173		s Sei	c Hi	s Ly:	s Pro	o Ph	e Arg	y Val	Lys
Ly:		e Me	t As	p Glı	n Val		n Glr	n Ala	a Se	r Al	a Se: 55	r Se	r Sei	Ala	Pro 1760

Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser Leu Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp Thr Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile

Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Pro Thr Ser Pro Val

Asp Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser Glu Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val Ser Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly Ser Pro Phe His Leu Thr Pro Asp Gln Glu Lys Pro Phe Thr Ser Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu Ile Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln

Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser

Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His Ser Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile

Ala Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser

Gly Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg

Val Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala

Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro

- Ser Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val 2580 2585 2590
- Asn Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala 2595 2600 2605
- Lys Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn 2610 2615 2620
- Ser Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser 2625 2630 2635 2640
- Lys Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp 2645 2650 2655
- Val Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly 2660 2665 2670
- Arg Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu 2675 2680 2685
- Lys Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln 2690 2695 2700
- Asn Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn 2705 2710 2715 2726
- Arg Leu Thr Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr 2725 2730 2735
- Glu Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn 2740 2745 2750
- Lys His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe 2770 2775 2780
- Asn Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala 2785 2790 2795 2800
- Arg Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Thr Lys Lys Arg 2805 2810 2815
- Asp Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys 2820 2825 2830
- Arg His Ser Gly Ser Tyr Leu Val Thr Ser Val 2835 2840

	(i)	(E	L) LE B) TY E) ST	NGTH PE: RAND	: 31 nucl	TERI 72 b eic SS: line	ase acid douk	pair l	rs.							
	(ii)	MOL	ECUL	E TY	PE:	cDNA	L									
	(vi)	ORI (A				: Homo	sap	iens	5							
(vii)	IMM (E				CE: . (TB2	:)									
		(E	A) NA B) LC	ME/K CATI	ON:	16		י ספי	ID NO							
GG3		_	-						ID NO		አሮአ	CCC	CCG	CCN	GGC	48
									Leu 10							40
									ATG Met							96
									GAC Asp							144
									ATC Ile							192
									TAT Tyr							240
									TAC Tyr 90							288
GAG Glu	AGT Ser	CCC Pro	AAC Asn	Lys	GAA Glu	GAT Asp	GAT Asp	ACC Thr	CAG Gln	TGG Trp	CTG Leu	ACC Thr	TAC Tyr 110	TGG Trp	GTA Val	336

(2) INFORMATION FOR SEQ ID NO:3:

GTG Val	TAT Tyr	GGT Gly 115	GTG Val	TTC Phe	AGC Ser	ATT Ile	GCT Ala 120	GAA Glu	TTC Phe	TTC Phe	TCT Ser	GAT Asp 125	ATC Ile	TTC Phe	CTG Leu	384
TCA Ser	TGG Trp 130	TTC Phe	CCC Pro	TTC Phe	TAC Tyr	TAC Tyr 135	ATG Met	CTG Leu	AAG Lys	TGT Cys	GGC Gly 140	TTC Phe	CTG Leu	TTG Leu	TGG Trp	432
TGC Cys 145	ATG Met	GCC Ala	CCG Pro	AGC Ser	CCT Pro 150	TCT Ser	AAT Asn	GGG Gly	GCT Ala	GAA Glu 155	CTG Leu	CTC Leu	TAC Tyr	AAG Lys	CGC Arg 160	480
ATC Ile	ATC Ile	CGT Arg	CCT Pro	TTC Phe 165	TTC Phe	CTG Leu	AAG Lys	CAC His	GAG Glu 170	TCC Ser	CAG Gln	ATG Met	GAC Asp	AGT Ser 175	GTG Val	528
GTC Val	AAG Lys	GAC Asp	CTT Leu 180	AAA Lys	GAC Asp	AAG Lys	TCC Ser	AAA Lys 185	GAG Glu	ACT Thr	GCA Ala	GAT Asp	GCC Ala 190	ATC Ile	ACT Thr	576
AAA Lys	GAA Glu	GCG Ala 195	Lys	AAA Lys	GCT Ala	ACC Thr	GTG Val 200	AAT Asn	TTA Leu	CTG Leu	GGT Gly	GAA Glu 205	Glu	AAG Lys	AAG Lys	624
	ACC Thr 210		ACCA	GAC	ТААА	CCAG	AC T	GGAT	GGAA	а ст	TCCT	GCCC	TCT	CTGT	ACC	680
TTC	CTAC	TGG	AGCT	TGAT	GT T	TATA	'TAGG	G AC	TGTG	GTAT	raa '	TTATT	ATT	ATAA	TGTTGC	740
CTI	'GGAA	ACA	TTTT	TGAG	AT A	AATT.	AGAT	T GG	STAAG	TGTT	GTA	AGTT	TCT	TTGC	TTACTT	800
TTA	.CTGT	CTA	TATA	TATA	GG G	AGCA	CTTI	'A AA	CTT	ATGC	AG	rggg	CAGT	GTCC	ACGTTT	860
TTC	GAA	ATG	TATT	TTGC	CT C	TGGG	TAGO	SA AA	\AGA'I	rgtat	GT.	rgcti	ATCC	TGC	GGAAAT	920
ATA	\AAC'l	AATT	AATA	raāa/	TA T	'ATAC	CCCZ	AC AC	GCT	GTGT	A CT	rtac:	rggg	CTCT	CCCTGC	980
ACC	SATT	TTC	TCTC	GTAGT	TA (CATT	raggi	RT AA	YTCT')TATI	G GT	rcta(CTTC	CTR	TAATGTA	1040
CAZ	YTTT:	rata	TAA	rtcn(GRA A	YTGT".	rttt	T A	GTAT'	rtgt(G CA	CATG'	TACA	TAT	GGAAATG	1100
TT	ACTG!	ГСТG	ACT	ACAN(CAT (CAT	CATG	CT C	ATGG(GGAG(G GA	GCAG(GGGA	AGG'	TTGTATG	1160
TG'	rcat'	TAT	AAC'	TTCT(GTA (CAGT	AAGA	CC A	CCTG	CCAA	a ag	CTGG.	AGGA	ACC	ATTGTGC	1220
TG	GTGT(GGTC	TAC'	TAAA'	TAA '	ract'	TTAG	GA A	ATAC	GTGA'	т та	АТАТ	GCAA	GTG.	AACAAAG	1280
TG.	AGAA.	ATGA	AAT	CGAA'	TGG .	AGAT'	TGGC	CT G	GTTG	TTTC	C GT	AGTA	TATG	GCA	TATGAAT	1340



ACCAGGATAG CTTTATAAAG CAGTTAGTTA GTTAGTTACT CACTCTAGTG ATAAATCGGG 1400 1460 AGTACCCTGT AACTCTCAAT TCCCTGAAAA ACTAGTAATA CTGTCTTATC TGCTATAAAC 1520 TTTACATATT TGTCTATTGT CAAGATGCTA CANTGGAMNC CATTTCTGGT TTTATCTTCA 1580 NAGSGGAGAN ACATGTTGAT TTAGTCTTCT TTCCCAATCT TCTTTTTTAA MCCAGTTTNA 1640 GGMNCTTCTG RAGATTTGYC CACCTCTGAT TACATGTATG TTCTYGTTTG TATCATKAGC 1700 AACAACATGC TAATGRCGAC ACCTAGCTCT RAGMGCAATT CTGGGAGANT GARAGGNWGT 1760 ATARAGTMNC CCATAATCTG CTTGGCAATA GTTAAGTCAA TCTATCTTCA GTTTTTCTCT 1820 GGCCTTTAAG GTCAAACACA AGAGGCTTCC CTAGTTTACA AGTCAGAGTC ACTTGTAGTC 1880 CATTTAAATG CCCTCATCCG TATTCTTTGT GTTGATAAGC TGCACAKGAC TACATAGTAA 1940 GTACAGANCA GTAAAGTTAA NNCGGATGTC TCCATTGATC TGCCAANTCG NTATAGAGAG 2000 CAATTTGTCT GGACTAGAAA ATCTGAGTTT TACACCATAC TGTTAAGAGT CCTTTTGAAT 2060 TAAACTAGAC TAAAACAAGT GTATAACTAA ACTAACAAGA TTAAATATCC AGCCAGTACA 2120 GTATTTTTTA AGGCAAATAA AGATGATTAG CTCACCTTGA GNTAACAATC AGGTAAGATC 2180 ATNACAATGT CTCATGATGT NAANAATATT AAAGATATCA ATACTAAGTG ACAGTATCAC 2240 NNCTAATATA ATATGGATCA GAGCATTTAT TTTGGGGAGG AAAACAGTGG TGATTACCGG 2300 CATTTTATTA AACTTAAAAC TTTGTAGAAA GCAAACAAAA TTGTTCTTGG GAGAAAATCA 2360 ACTTTTAGAT TAAAAAAATT TTAAGTAWCT AGGAGTATTT AAATCCTTTT CCCATAAATA 2420 AAAGTACAGT TTTCTTGGTG GCAGAATGAA AATCAGCAAC NTCTAGCATA TAGACTATAT 2480 AATCAGATTG ACAGCATATA GAATATATTA TCAGACAAGA TGAGGAGGTA CAAAAGTTAC 2540 TATTGCTCAT AATGACTTAC AGGCTAAAAN TAGNTNTAAA ATACTATATT AAATTCTGAA 2600 TGCAATTTTT TTTTGTTCCC TTGAGACCAA AATTTAAGTT AACTGTTGCT GGCAGTCTAA 2660 GTGTAAATGT TAACAGCAGG AGAAGTTAAG AATTGAGCAG TTCTGTTGCA TGATTTCCCA 2720 AATGAAATAC TGCCTTGGCT AGAGTTTGAA AAACTAATTG AGCCTGTGCC TGGCTAGAAA 2780 ACAAGCGTTT ATTTGAATGT GAATAGTGTT TCAAAGGTAT GTAGTTACAG AATTCCTACC 2840 AAACAGCTTA AATTCTTCAA GAAAGAATTC CTGCAGCAGT TATTCCCTTA CCTGAAGGCT 2900



TCAATCATTT GGATCAACAA CTGCTACTCT CGGGA	AGACT CCTCTACTCA CAGCTGAAGA 2960
AAATGAGCAC ACCCTTCACA CTGTTATCAC CTATC	
AATAAATAGA TGTAAATAAA ATTGAGWTCT CATTT	
AAATGACCTC ATGTTGTGGT TTAAACAGCA ACTGC	
ANCCTATATA TACATCTCTG TCAGTGCCCC TC	3172
(2) INFORMATION FOR SEQ ID NO:4: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 210 amino acid (B) TYPE: amino acid (D) TOPOLOGY: linear	ids
(ii) MOLECULE TYPE: protein	
(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:4:
Ala Val Ala Ala Pro Val Tyr Pro Ala L 1 5	eu Gly Thr Ala Pro Gly Gly 10 15
Glu Thr Val Pro Ala Met Ser Ala Ala M 20 25	et Arg Glu Arg Phe Asp Arg 30
Phe Leu His Glu Lys Asn Cys Met Thr A 35 40	sp Leu Leu Ala Lys Leu Glu 45
Ala Lys Thr Gly Val Asn Arg Ser Phe I 50 55	le Ala Leu Gly Val Ile Gly 60
Leu Val Ala Leu Tyr Leu Val Phe Gly 7 65 70	Tyr Gly Ala Ser Leu Leu Cys 75 80
Asn Leu Ile Gly Phe Gly Tyr Pro Ala 7	Tyr Ile Ser Ile Lys Ala Ile 90 95
Glu Ser Pro Asn Lys Glu Asp Asp Thr	Gln Trp Leu Thr Tyr Trp Val 110
Val Tyr Gly Val Phe Ser Ile Ala Glu 115 120	Phe Phe Ser Asp Ile Phe Leu 125
Ser Trp Phe Pro Phe Tyr Tyr Met Leu 130 135	Lys Cys Gly Phe Leu Leu Trp 140

Cys Met Ala Pro Ser Pro Ser Asn Gly Ala Glu Leu Leu Tyr Lys Arg 150 Ile Ile Arg Pro Phe Phe Leu Lys His Glu Ser Gln Met Asp Ser Val 170 Val Lys Asp Leu Lys Asp Lys Ser Lys Glu Thr Ala Asp Ala Ile Thr 185 180 Lys Glu Ala Lys Lys Ala Thr Val Asn Leu Leu Gly Glu Glu Lys Lys 200 Ser Thr 210 (2) INFORMATION FOR SEQ ID NO:5: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 434 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (vii) IMMEDIATE SOURCE: (B) CLONE: TB1 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5: Val Ala Pro Val Val Val Gly Ser Gly Arg Ala Pro Arg His Pro Ala 10 5 Pro Ala Ala Met His Pro Arg Pro Asp Gly Phe Asp Gly Leu Gly 20 Tyr Arg Gly Gly Ala Arg Asp Glu Gln Gly Phe Gly Gly Ala Phe Pro Ala Arg Ser Phe Ser Thr Gly Ser Asp Leu Gly His Trp Val Thr Thr 50 Pro Pro Asp Ile Pro Gly Ser Arg Asn Leu His Trp Gly Glu Lys Ser 75 70

Pro Pro Tyr Gly Val Pro Thr Thr Ser Thr Pro Tyr Glu Gly Pro Thr 85 90 95	
Glu Glu Pro Phe Ser Ser Gly Gly Gly Gly Ser Val Gln Gly Gln Ser 100 105 110	•
Ser Glu Gln Leu Asn Arg Phe Ala Gly Phe Gly Ile Gly Leu Ala Ser 115 120 125	<i>:</i>
Leu Phe Thr Glu Asn Val Leu Ala His Pro Cys Ile Val Leu Arg Arg 130 135 140	3
Gln Cys Gln Val Asn Tyr His Ala Gln His Tyr His Leu Thr Pro Pho 145 150 155 160	e 0
Thr Val Ile Asn Ile Met Tyr Ser Phe Asn Lys Thr Gln Gly Pro Are 165 170 175	g
Ala Leu Trp Lys Gly Met Gly Ser Thr Phe Ile Val Gln Gly Val Th 180 185 190	r
Leu Gly Ala Glu Gly Ile Ile Ser Glu Phe Thr Pro Leu Pro Arg Gl 195 200 205	.u
Val Leu His Lys Trp Ser Pro Lys Gln Ile Gly Glu His Leu Leu Le 210 215 220)u
Lys Ser Leu Thr Tyr Val Val Ala Met Pro Phe Tyr Ser Ala Ser Le 225 230 235 24	eu 40
Ile Glu Thr Val Gln Ser Glu Ile Ile Arg Asp Asn Thr Gly Ile Le 245 250 255	eu
Glu Cys Val Lys Glu Gly Ile Gly Arg Val Ile Gly Met Gly Val P 260 265 270	ro
His Ser Lys Arg Leu Leu Pro Leu Leu Ser Leu Ile Phe Pro Thr V 275 280 285	al
Leu His Gly Val Leu His Tyr Ile Ile Ser Ser Val Ile Gln Lys P 290 295 300	he
Val Leu Leu Ile Leu Lys Arg Lys Thr Tyr Asn Ser His Leu Ala G 305 310 315	31u 320
Ser Thr Ser Pro Val Gln Ser Met Leu Asp Ala Tyr Phe Pro Glu I 325 330 335	⊿eu
Ile Ala Asn Phe Ala Ala Ser Leu Cys Ser Asp Val Ile Leu Tyr I 340 345 350	Pro

Leu Glu Thr Val Leu His Arg Leu His Ile Gln Gly Thr Arg Thr Ile Ile Asp Asn Thr Asp Leu Gly Tyr Glu Val Leu Pro Ile Asn Thr Gln 375 Tyr Glu Gly Met Arg Asp Cys Ile Asn Thr Ile Arg Gln Glu Gly 395 390 385 Val Phe Gly Phe Tyr Lys Gly Phe Gly Ala Val Ile Ile Gln Tyr Thr 410 405 Leu His Ala Ala Val Leu Gln Ile Thr Lys Ile Ile Tyr Ser Thr Leu 420 Leu Gln (2) INFORMATION FOR SEQ ID NO:6: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 185 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: protein (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (vii) IMMEDIATE SOURCE: (B) CLONE: YS-39 (TB2) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Glu Leu Arg Arg Phe Asp Arg Phe Leu His Glu Lys Asn Cys Met Thr 10 5

Asp Leu Leu Ala Lys Leu Glu Ala Lys Thr Gly Val Asn Arg Ser Phe 20 25

Ile Ala Leu Gly Val Ile Gly Leu Val Ala Leu Tyr Leu Val Phe Gly 35

Tyr Gly Ala Ser Leu Leu Cys Asn Leu Ile Gly Phe Gly Tyr Pro Ala 50 55 60

Tyr Ile Ser Ile Lys Ala Ile Glu Ser Pro Asn Lys Glu Asp Asp Thr 70 Gln Trp Leu Thr Tyr Trp Val Val Tyr Gly Val Phe Ser Ile Ala Glu Phe Phe Ser Asp Ile Phe Leu Ser Trp Phe Pro Phe Tyr Tyr Ile Leu 105 Lys Cys Gly Phe Leu Leu Trp Cys Met Ala Pro Ser Pro Ser Asn Gly 120 Ala Glu Leu Leu Tyr Lys Arg Ile Ile Arg Pro Phe Phe Leu Lys His 130 Glu Ser Gln Met Asp Ser Val Val Lys Asp Leu Lys Asp Lys Ala Lys 150 Glu Thr Ala Asp Ala Ile Thr Lys Glu Ala Lys Lys Ala Thr Val Asn 170 165 Leu Leu Gly Glu Glu Lys Lys Ser Thr 180 (2) INFORMATION FOR SEQ ID NO:7: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: [2842] <u>2843</u> amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Homo sapiens
- (vii) IMMEDIATE SOURCE:
 - (B) CLONE: APC
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met Ala Ala Ser Tyr Asp Gln Leu Leu Lys Gln Val Glu Ala Leu 5

Lys Met Glu Asn Ser Asn Leu Arg Gln Glu Leu Glu Asp Asn Ser Asn 25 20

His Leu Thr Lys Leu Glu Thr Glu Ala Ser Asn Met Lys Glu Val Leu 35 40 45

Lys Gln Leu Gln Gly Ser Ile Glu Asp Glu Ala Met Ala Ser Ser Gly 50 55

Gln Ile Asp Leu Leu Glu Arg Leu Lys Glu Leu Asn Leu Asp Ser Ser 65 70 75 80

Asn Phe Pro Gly Val Lys Leu Arg Ser Lys Met Ser Leu Arg Ser Tyr 85 90 95

Gly Ser Arg Glu Gly Ser Val Ser Ser Arg Ser Gly Glu Cys Ser Pro 100 105 110

Val Pro Met Gly Ser Phe Pro Arg Arg Gly Phe Val Asn Gly Ser Arg 115 120 125

Glu Ser Thr Gly Tyr Leu Glu Glu Leu Glu Lys Glu Arg Ser Leu Leu 130 135 140

Leu Ala Asp Leu Asp Lys Glu Glu Lys Glu Lys Asp Trp Tyr Tyr Ala 145 150 150 155 160

Gln Leu Gln Asn Leu Thr Lys Arg Ile Asp Ser Leu [Leu Thr Glu Asn 165 170 175

Phe Ser Leu Gln Thr Asp Met Thr Arg Arg Gln Leu Glu Tyr Glu Ala 180 185 190

Arg Gln Ile Arg Val Ala Met Glu Glu Gln Leu Gly Thr Cys Gln Asp 195 200 205

Met Glu Lys Arg Ala Gln Arg Arg Ile Ala Arg Ile Gln Gln Ile Glu 210 215 220

Lys Asp Ile Leu Arg Ile Arg Gln Leu Leu Gln Ser Gln Ala Thr Glu 225 230 230 240

Ala Glu Arg Ser Ser Gln Asn Lys His Glu Thr Gly Ser His Asp Ala 245 250 255

Glu Arg Gln Asn Glu Gly Gln Gly Val Gly Glu Ile Asn Met Ala Thr 260 265 270

Ser Gly Asn Gly Gln Gly Ser Thr Thr Arg Met Asp His Glu Thr Ala 275 280 285

Ser Val Leu Ser Ser Ser Ser Thr His Ser Ala Pro Arg Arg Leu Thr 290 295 300

Ser 305	His	Leu	Gly	Thr	Lys 310	Val	Glu	Met	Val	Tyr 315	Ser	Leu	Leu	Ser	Met 320
Leu	Gly	Thr	His	Asp 325	Lys	Asp	Asp	Met	Ser 330	Arg	Thr	Leu	Leu	Ala 335	Met
Ser	Ser	Ser	Gln 340	Asp	Ser	Cys	Ile	Ser 345	Met	Arg	Gln	Ser	Gly 350	Cys	Leu
Pro	Leu	Leu 355	Ile	Gln	Leu	Leu	His 360	Gly	Asn	Asp	Lys	Asp 365	Ser	Val	Leu
Leu	Gly 370	Asn	Ser	Arg	Gly	Ser 375	Lys	Glu	Ala	Arg	Ala 380	Arg	Ala	Ser	Ala
Ala 385	Leu	His	Asn	Ile	Ile 390	His	Ser	Gln	Pro	Asp 395	Asp	Lys	Arg	Gly	Arg 400
Arg	Glu	Ile	Arg	Val 405	Leu	His	Leu	Leu	Glu 410	Gln	Ile	Arg	Ala	Tyr 415	Cys
Glu	Thr	Cys	Trp 420	Glu	Trp	Gln	Glu	Ala 425	His	Glu	Pro	Gly	Met 430	Asp	Gln
Asp	Lys	Asn 435	Pro	Met	Pro	Ala	Pro 440	Val	Glu	His	Gln	Ile 445	Cys	Pro	Ala
Val	Cys 450		Leu	Met	Lys	Leu 455		Phe	Asp	Glu	Glu 460	His	Arg	His	Ala
Met 465		Glu	Leu	Gly	Gly 470	Leu	Gln	Ala	Ile	Ala 475	Glu	Leu	Leu	Gln	Val 480
Asp	Cys	Glu	Met	Tyr 485		Leu	Thr	Asn	Asp 490	His	Tyr	Ser	Ile	Thr 495	Leu
Arg	Arg		Ala 500		Met	Ala	. Leu	Thr 505		. Leu	Thr	Phe	Gly 510	Asp	Val
Ala	. Asr	Lys 515		Thr	Leu	Cys	s Ser 520	Met	. Lys	Gly	Cys	Met 525	Arg	, Ala	Leu
Val	Ala 530		ı Lev	ı Lys	s Ser	Glu 535	ı Ser	Glu	a Asp	Leu	Gln 540	Gln	ı Val	Ile	e Ala
Sei 545	_	L Le	ı Arç	j Ası	n Leu 55(c Trg	Arg	g Ala	a Asp 555	Val	. Asr	ı Sei	C Lys	560
Thi	r Lei	ı Ar	g Glı	ı Va: 56!		y Sei	r Val	L Lys	5 Ala	a Leu)	ı Met	: Glı	і Су	s Ala 57	a Leu 5

Glu Val Lys Lys Glu Ser Thr Leu Lys Ser Val Leu Ser Ala Leu Trp Asn Leu Ser Ala His Cys Thr Glu Asn Lys Ala Asp Ile Cys Ala Val Asp Gly Ala Leu Ala Phe Leu Val Gly Thr Leu Thr Tyr Arg Ser Gln Thr Asn Thr Leu Ala Ile Ile Glu Ser Gly Gly Gly Ile Leu Arg Asn Val Ser Ser Leu Ile Ala Thr Asn Glu Asp His Arg Gln Ile Leu Arg Glu Asn Asn Cys Leu Gln Thr Leu Leu Gln His Leu Lys Ser His Ser Leu Thr Ile Val Ser Asn Ala Cys Gly Thr Leu Trp Asn Leu Ser Ala Arg Asn Pro Lys Asp Gln Glu Ala Leu Trp Asp Met Gly Ala Val Ser Met Leu Lys Asn Leu Ile His Ser Lys His Lys Met Ile Ala Met Gly Ser Ala Ala Ala Leu Arg Asn Leu Met Ala Asn Arg Pro Ala Lys Tyr Lys Asp Ala Asn Ile Met Ser Pro Gly Ser Ser Leu Pro Ser Leu His Val Arg Lys Gln Lys Ala Leu Glu Ala Glu Leu Asp Ala Gln His Leu Ser Glu Thr Phe Asp Asn Ile Asp Asn Leu Ser Pro Lys Ala Ser His Arg Ser Lys Gln Arg His Lys Gln Ser Leu Tyr Gly Asp Tyr Val Phe Asp Thr Asn Arg His Asp Asp Asn Arg Ser Asp Asn Phe Asn Thr Gly Asn Met Thr Val Leu Ser Pro Tyr Leu Asn Thr Thr Val Leu Pro Ser Ser Ser Ser Ser Arg Gly Ser Leu Asp Ser Ser Arg Ser Glu Lys Asp

Arg Ser Leu Glu Arg Glu Arg Gly Ile Gly Leu Gly Asn Tyr His Pro Ala Thr Glu Asn Pro Gly Thr Ser Ser Lys Arg Gly Leu Gln Ile Ser Thr Thr Ala Ala Gln Ile Ala Lys Val Met Glu Glu Val Ser Ala Ile His Thr Ser Gln Glu Asp Arg Ser Ser Gly Ser Thr Thr Glu Leu His Cys Val Thr Asp Glu Arg Asn Ala Leu Arg Arg Ser Ser Ala Ala His Thr His Ser Asn Thr Tyr Asn Phe Thr Lys Ser Glu Asn Ser Asn Arg Thr Cys Ser Met Pro Tyr Ala Lys Leu Glu Tyr Lys Arg Ser Ser Asn Asp Ser Leu Asn Ser Val Ser Ser Ser Asp Gly Tyr Gly Lys Arg Gly Gln Met Lys Pro Ser Ile Glu Ser Tyr Ser Glu Asp Asp Glu Ser Lys Phe Cys Ser Tyr Gly Gln Tyr Pro Ala Asp Leu Ala His Lys Ile His Ser Ala Asn His Met Asp Asp Asn Asp Gly Glu Leu Asp Thr Pro Ile Asn Tyr Ser Leu Lys Tyr Ser Asp Glu Gln Leu Asn Ser Gly Arg Gln Ser Pro Ser Gln Asn Glu Arg Trp Ala Arg Pro Lys His Ile Ile Glu Asp Glu Ile Lys Gln Ser Glu Gln Arg Gln Ser Arg Asn Gln Ser Thr Thr Tyr Pro Val Tyr Thr Glu Ser Thr Asp Asp Lys His Leu Lys Phe Gln Pro His Phe Gly Gln Gln Glu Cys Val Ser Pro Tyr Arg Ser Arg Gly Ala Asn Gly Ser Glu Thr Asn Arg Val Gly Ser Asn His Gly Ile

Asn Gln Asn Val Ser Gln Ser Leu Cys Gln Glu Asp Asp Tyr Glu Asp Asp Lys Pro Thr Asn Tyr Ser Glu Arg Tyr Ser Glu Glu Glu Gln His Glu Glu Glu Glu Arg Pro Thr Asn Tyr Ser Ile Lys Tyr Asn Glu Glu Lys Arg His Val Asp Gln Pro Ile Asp Tyr Ser Leu Lys Tyr Ala Thr Asp Ile Pro Ser Ser Gln Lys Gln Ser Phe Ser Phe Ser Lys Ser Ser Ser Gly Gln Ser Ser Lys Thr Glu His Met Ser Ser Ser Glu Asn Thr Ser Thr Pro Ser Ser Asn Ala Lys Arg Gln Asn Gln Leu His Pro Ser Ser Ala Gln Ser Arg Ser Gly Gln Pro Gln Lys Ala Ala Thr Cys Lys Val Ser Ser Ile Asn Gln Glu Thr Ile Gln Thr Tyr Cys Val Glu Asp Thr Pro Ile Cys Phe Ser Arg Cys Ser Ser Leu Ser Ser Leu Ser Ser Ala Glu Asp Glu Ile Gly Cys Asn Gln Thr Thr Gln Glu Ala Asp Ser Ala Asn Thr Leu Gln Ile Ala Glu Ile Lys Glu Lys Ile Gly Thr Arg Ser Ala Glu Asp Pro Val Ser Glu Val Pro Ala Val Ser Gln His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glu Ser Ala Arg His Lys Ala Val Glu Phe Ser Ser Gly Ala Lys Ser Pro Ser Lys Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Val Gln Glu Thr Pro Leu Met Phe Ser Arg Cys Thr Ser Val Ser Ser Leu

Asp Ser Phe Glu Ser Arg Ser Ile Ala Ser Ser Val Gln Ser Glu Pro 1395 1400 1405

Cys Ser Gly Met Val Ser Gly Ile Ile Ser Pro Ser Asp Leu Pro Asp 1410 1415 1420

Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro Pro 1425 1430 1435 1440

Pro Pro Gln Thr Ala Gln Thr Lys Arg Glu Val Pro Lys Asn Lys Ala 1445 1450 1455

Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val Asn 1460 1465 1470

Ala Ala Val Gln Arg Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu 1475 1480 1485

His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser 1490 1495 1500

Leu Ser Ala Leu Ser Leu Asp Glu Pro Phe Ile Gln Lys Asp Val Glu 1505 1510 1515 1520

Leu Arg Ile Met Pro Pro Val Gln Glu Asn Asp Asn Gly Asn Glu Thr 1525 1530 1535

Glu Ser Glu Gln Pro Lys Glu Ser Asn Glu Asn Gln Glu Lys Glu Ala 1540 1545 1550

Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp Asp 1555 1560 1565

Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr 1570 1575 1580

Lys Ser Ser Arg Lys Ala Lys Lys Pro Ala Gln Thr Ala Ser Lys Leu 1585 1590 1595 1600

Pro Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu 1605 1610 1615

Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe Thr 1620 1625 1630

Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro Ile 1635 1640 1645

Asn Phe Ser Thr Ala Thr Ser Leu Ser Asp Leu Thr Ile Glu Ser Pro 1650 1655 1660 Pro Asn Glu Leu Ala Ala Gly Glu Gly Val Arg Gly Gly Ala Gln Ser Gly Glu Phe Glu Lys Arg Asp Thr Ile Pro Thr Glu Gly Arg Ser Thr Asp Glu Ala Gln Gly Gly Lys Thr Ser Ser Val Thr Ile Pro Glu Leu Asp Asp Asn Lys Ala Glu Glu Gly Asp Ile Leu Ala Glu Cys Ile Asn Ser Ala Met Pro Lys Gly Lys Ser His Lys Pro Phe Arg Val Lys Lys Ile Met Asp Gln Val Gln Gln Ala Ser Ala Ser Ser Ser Ala Pro Asn Lys Asn Gln Leu Asp Gly Lys Lys Lys Pro Thr Ser Pro Val Lys Pro Ile Pro Gln Asn Thr Glu Tyr Arg Thr Arg Val Arg Lys Asn Ala Asp Ser Lys Asn Asn Leu Asn Ala Glu Arg Val Phe Ser Asp Asn Lys Asp Ser Lys Lys Gln Asn Leu Lys Asn Asn Ser Lys Asp Phe Asn Asp Lys Leu Pro Asn Asn Glu Asp Arg Val Arg Gly Ser Phe Ala Phe Asp Ser Pro His His Tyr Thr Pro Ile Glu Gly Thr Pro Tyr Cys Phe Ser Arg Asn Asp Ser Leu Ser Ser Leu Asp Phe Asp Asp Asp Val Asp Leu Ser Arg Glu Lys Ala Glu Leu Arg Lys Ala Lys Glu Asn Lys Glu Ser Glu Ala Lys Val Thr Ser His Thr Glu Leu Thr Ser Asn Gln Gln Ser Ala Asn Lys Thr Gln Ala Ile Ala Lys Gln Pro Ile Asn Arg Gly Gln Pro Lys Pro Ile Leu Gln Lys Gln Ser Thr Phe Pro Gln Ser Ser

Lys Asp Ile Pro Asp Arg Gly Ala Ala Thr Asp Glu Lys Leu Gln Asn 1940 1945 1950

Phe Ala Ile Glu Asn Thr Pro Val Cys Phe Ser His Asn Ser Ser Leu 1955 1960 1965

Ser Ser Leu Ser Asp Ile Asp Gln Glu Asn Asn Asn Lys Glu Asn Glu 1970 1975 1980

Pro Ile Lys Glu Thr Glu Pro Pro Asp Ser Gln Gly Glu Pro Ser Lys 1985 1990 1995 2000

Pro Gln Ala Ser Gly Tyr Ala Pro Lys Ser Phe His Val Glu Asp Thr 2005 2010 2015

Pro Val Cys Phe Ser Arg Asn Ser Ser Leu Ser Ser Leu Ser Ile Asp 2020 2025 2030

Ser Glu Asp Asp Leu Leu Gln Glu Cys Ile Ser Ser Ala Met Pro Lys 2035 2040 2045

Lys Lys Lys Pro Ser Arg Leu Lys Gly Asp Asn Glu Lys His Ser Pro 2050 2055 2060

Arg Asn Met Gly Gly Ile Leu Gly Glu Asp Leu Thr Leu Asp Leu Lys 2065 2070 2075 2080

Asp Ile Gln Arg Pro Asp Ser Glu His Gly Leu Ser Pro Asp Ser Glu 2085 2090 2095

Asn Phe Asp Trp Lys Ala Ile Gln Glu Gly Ala Asn Ser Ile Val Ser 2100 2105 2110

Ser Leu His Gln Ala Ala Ala Ala Cys Leu Ser Arg Gln Ala Ser 2115 2120 2125

Ser Asp Ser Asp Ser Ile Leu Ser Leu Lys Ser Gly Ile Ser Leu Gly 2130 2135 2140

Ser Pro Phe His Leu Thr Pro Asp Gln Glu Glu Lys Pro Phe Thr Ser 2145 2150 2155 2160

Asn Lys Gly Pro Arg Ile Leu Lys Pro Gly Glu Lys Ser Thr Leu Glu 2165 2170 2175

Thr Lys Lys Ile Glu Ser Glu Ser Lys Gly Ile Lys Gly Gly Lys Lys 2180 2185 2190

Val Tyr Lys Ser Leu Ile Thr Gly Lys Val Arg Ser Asn Ser Glu Ile 2195 2200 2205 Ser Gly Gln Met Lys Gln Pro Leu Gln Ala Asn Met Pro Ser Ile Ser Arg Gly Arg Thr Met Ile His Ile Pro Gly Val Arg Asn Ser Ser Ser Ser Thr Ser Pro Val Ser Lys Lys Gly Pro Pro Leu Lys Thr Pro Ala Ser Lys Ser Pro Ser Glu Gly Gln Thr Ala Thr Thr Ser Pro Arg Gly Ala Lys Pro Ser Val Lys Ser Glu Leu Ser Pro Val Ala Arg Gln Thr Ser Gln Ile Gly Gly Ser Ser Lys Ala Pro Ser Arg Ser Gly Ser Arg Asp Ser Thr Pro Ser Arg Pro Ala Gln Gln Pro Leu Ser Arg Pro Ile Gln Ser Pro Gly Arg Asn Ser Ile Ser Pro Gly Arg Asn Gly Ile Ser Pro Pro Asn Lys Leu Ser Gln Leu Pro Arg Thr Ser Ser Pro Ser Thr Ala Ser Thr Lys Ser Ser Gly Ser Gly Lys Met Ser Tyr Thr Ser Pro Gly Arg Gln Met Ser Gln Gln Asn Leu Thr Lys Gln Thr Gly Leu Ser Lys Asn Ala Ser Ser Ile Pro Arg Ser Glu Ser Ala Ser Lys Gly Leu Asn Gln Met Asn Asn Gly Asn Gly Ala Asn Lys Lys Val Glu Leu Ser Arg Met Ser Ser Thr Lys Ser Ser Gly Ser Glu Ser Asp Arg Ser Glu Arg Pro Val Leu Val Arg Gln Ser Thr Phe Ile Lys Glu Ala Pro Ser Pro Thr Leu Arg Arg Lys Leu Glu Glu Ser Ala Ser Phe Glu Ser Leu Ser Pro Ser Ser Arg Pro Ala Ser Pro Thr Arg Ser Gln Ala Gln Thr

Pro Val Leu Ser Pro Ser Leu Pro Asp Met Ser Leu Ser Thr His Ser 2485 2490 2495

Ser Val Gln Ala Gly Gly Trp Arg Lys Leu Pro Pro Asn Leu Ser Pro 2500 2505 2510

Thr Ile Glu Tyr Asn Asp Gly Arg Pro Ala Lys Arg His Asp Ile Ala 2515 2520 2525

Arg Ser His Ser Glu Ser Pro Ser Arg Leu Pro Ile Asn Arg Ser Gly 2530 2540

Thr Trp Lys Arg Glu His Ser Lys His Ser Ser Ser Leu Pro Arg Val 2545 2550 2555 2560

Ser Thr Trp Arg Arg Thr Gly Ser Ser Ser Ser Ile Leu Ser Ala Ser 2565 2570 2575

Ser Glu Ser Ser Glu Lys Ala Lys Ser Glu Asp Glu Lys His Val Asn 2580 2585 2590

Ser Ile Ser Gly Thr Lys Gln Ser Lys Glu Asn Gln Val Ser Ala Lys 2595 2600 2605

Gly Thr Trp Arg Lys Ile Lys Glu Asn Glu Phe Ser Pro Thr Asn Ser 2610 2615 2620

Thr Ser Gln Thr Val Ser Ser Gly Ala Thr Asn Gly Ala Glu Ser Lys 2625 2630 2635 2640

Thr Leu Ile Tyr Gln Met Ala Pro Ala Val Ser Lys Thr Glu Asp Val 2645 2650 2655

Trp Val Arg Ile Glu Asp Cys Pro Ile Asn Asn Pro Arg Ser Gly Arg 2660 2665 2670

Ser Pro Thr Gly Asn Thr Pro Pro Val Ile Asp Ser Val Ser Glu Lys 2675 2680 2685

Ala Asn Pro Asn Ile Lys Asp Ser Lys Asp Asn Gln Ala Lys Gln Asn 2690 2695 2700

Val Gly Asn Gly Ser Val Pro Met Arg Thr Val Gly Leu Glu Asn Arg 2705 2710 2715 2720

Leu Asn Ser Phe Ile Gln Val Asp Ala Pro Asp Gln Lys Gly Thr Glu 2725 2730 2735

Ile Lys Pro Gly Gln Asn Asn Pro Val Pro Val Ser Glu Thr Asn Glu 2740 2745 2750

Ser Ser Ile Val Glu Arg Thr Pro Phe Ser Ser Ser Ser Ser Lys 2755 2760 2765

His Ser Ser Pro Ser Gly Thr Val Ala Ala Arg Val Thr Pro Phe Asn 2770 2775 2780

Tyr Asn Pro Ser Pro Arg Lys Ser Ser Ala Asp Ser Thr Ser Ala Arg 2785 2790 2795 2800

Pro Ser Gln Ile Pro Thr Pro Val Asn Asn Asn Thr Lys Lys Arg Asp 2805 2810 2815

Ser Lys Thr Asp Ser Thr Glu Ser Ser Gly Thr Gln Ser Pro Lys Arg 2820 2825 2830

His Ser Gly Ser Tyr Leu Val Thr Ser Val 2835 2840]

												Pro	Leu	Thr	Glu
														<u> 175</u>	
Asn	Phe	Ser	Leu	Gln	Thr	Asp	Met	Thr	Arg	Arg	Gln	Leu	Glu	Tyr	<u>Glu</u>
			180					185					<u> 190</u>		
Ala	Arg	Gln	Ile	Arg	Val	Ala	Met	Glu	Glu	Gln	Leu	Gly	Thr	Cys	Gln
		195					200					205			
Asp	Met	Glu	Lys	Arg	Ala	Gln	Arg	Arg	Ile	Ala	Arg	Ile	Gln	Gln	Ile
	210					215					220				
Glu	Lys	Asp	Ile	Leu	Arg	Ile	Arg	Gln	Leu	Leu	Gln	Ser	Gln	Ala	Thr
225					230					235					240
Glu	Ala	Glu	Arg	Ser	Ser	Gln	Asn	Lys	His	Glu	Thr	Gly	Ser	His	Asp
				245					250					255	
Ala	Glu	Arg	Gln	Asn	Glu	Gly	Gln	Gly	Val	Gly	Glu	Ile	Asn	Met	<u>Ala</u>
			260					265					270		
Thr	Ser	Gly	Asn	Gly	Gln	Gly	Ser	Thr	Thr	Arg	Met	Asp	His	Glu	Thr
		275					280					285			
Ala	Ser	Val	Leu	Ser	Ser	Ser	Ser	Thr	His	Ser	Ala	Pro	Arg	Arg	Leu
	290					295					<u> 300</u>				
Thr	Ser	His	Leu	Gly	Thr	Lys	Val	Glu	Met	Va1	Tyr	Ser	Leu	Leu	Ser
305					310					315					320
Met	Leu	Gly	Thr	His	Asp	Lys	Asp	Asp	Met	Ser	Arg	Thr	Leu	Leu	<u>Ala</u>
				325					330					335	
Met	Ser	Ser	Ser	Gln	Asp	Ser	Cys	Ile	Ser	Met	Arg	<u>Gln</u>	Ser	Gly	Cys
			340					345					350		
Leu	Pro	Leu	Leu	Ile	Gln	Leu	Leu	His	Gly	Asn	Asp		Asp	<u>Ser</u>	<u>Val</u>
		355					360					365		_	_
Leu	Leu	Gly	Asn	Ser	Arg	Gly	Ser	Lys	Glu	Ala	Arg	Ala	Arg	Ala	Ser
	370					375					380				
Ala	Ala	Leu	His	Asn	Ile	Ile	<u>His</u>	Ser	Gln	Pro	Asp	Asp	Lys	Arg	Gly
385					390					395					400
Arg	Arg	Glu	Ile	Arg	Val	Leu	<u>His</u>	Leu			Gln	Ile	Arg	Ala	Tyr
				405					410					415	•
Cys	Glu	Thr	Cys	Trp	Glu	Trp	Gln	Glu	Ala	His	Glu	Pro	Gly	Met	Asp

			420					425					430		
Gln	Asp	Lvs		Pro	Met	Pro	Ala		Val	Glu	His	Gln		Cys	Pro
<u> </u>		435					440					445			
Ala	Va1		Val	Leu	Met	Lvs		Ser	Phe	Asp	Glu		His	Arq	His
	450	-2-				455					460				
Ala		Asn	Glu	Leu	Gly		Leu	Gln	Ala	Ile		Glu	Leu	Leu	Gln
465		11011	014		470	<u> </u>				475					480
	Asn	Cvs	Glu	Met	Tyr	Glv	Leu	Thr	Asn		His	Tvr	Ser	Ile	Thr
<u> </u>	7100	Cyb	014	485	-7-	017			490	****			~~-	495	
T.611	Δrα	Δησ	Tyr		Gly	Met	Δla	T.eu		Asn	Leu	Thr	Phe		Asp
пец	Arg	arg	500	піц	OLY	ricc	AIG	505	1111				510	<u> </u>	<u> </u>
1727	λla	λαn		λ1 ລ	Thr	T.011	Cvc		Mot	Lare	Glv	Cve		Δτα	Δla
vai	Ата	515	шуъ	Ата	1114	<u>nea</u>	520	DCI	HCC	<u> </u>	OLY	525	1100	1119	
T 011	1707		Cln	T 011	Lys	Sor	-	Sor	G111	λen	T.A11		Gln	Val	T10
Беп	530	Ата	GIII	пеп	пуs	535	Giu	per	GIU	Дад	540	GIII	GIII	var	110
71-		7707	T 011	7 200	Asn		Cor	m~~	7 ~~	717		17-1	λcn	Car	Lvc
	Ser	vai	ьeu	Arg	550	пеп	ser	пр	Arg	555	Asp	<u>vaı</u>	ASII	SET	560
545	mb	T 011	7	01		C1	Cox	1701	Tara		T 011	Mot	Clu	Cvc	
ьуs	THE	ьeu	Arg	565	Val	СТУ	Ser	vai	570	Ата	пеп	Met	GIU	575	Ala
T	G1	77-1	T = ===		G1	Com	mb -c	T 011		Cox	17-1	T 011	Cor		T 011
Leu	GIU	Val		пĀR	Glu	Ser	1111		пĀВ	ser	vai	neu		Ala	пец
			580				m1	585	3	T	77-	7	590	O	710
Trp	Asn		Ser	Ата	His	Cys		GIU	Asn	цуs	Ата		тте	Cys	Ala
		595			- 1		600	77-7	01	m1	T	605	m	7	C
<u>val</u>		Gly	Ala	Leu	Ala		Leu	Val	GIA	Thr		Thr	Tyr	Arg	ser
	610					615		~1		~1	620	01	- 1 -	.	3
	Thr	Asn	Thr	Leu	Ala	ше	тте	GIU	Ser		GIA	GIA	тте	ьeu	
625					630				~ 3	635			<u> </u>	- 1.	640
Asn	Val	Ser	Ser		Ile	Ala	Thr	Asn		Asp	HIS	Arg	GIn		ьeu
				645			1		650			Ŧ.	T	655	***
Arg	GLu	Asn		Cys	Leu	GIn	Thr		Ļеu	GIn	HIS	ьеu		Ser	HIS
			660					665	~ 1				<u>670</u>	_	~
Ser	Leu		Ile	Val	Ser	Asn		Cys	GLY	Thr	Leu		Asn	Leu	Ser
		675					680					685	~1		1
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	690	***				695					700				
	Met	Leu	Lys	Asn	Leu	Ile	His	Ser	Lys		Lys	Met	lle	Ala	
<u>705</u>					710					715					720
Gly	Ser	Ala	Ala		Leu	Arg	Asn	Leu		Ala	Asn	Arg	Pro		Lys
		- 1/1		725					730					<u>735</u>	_
Tyr	Lys	Asp		Asn	Ile	Met	Ser		Gly	Ser	Ser	Leu		Ser	Leu
			740					745					750		
His	Val		Lys	Gln	Lys	Ala		Glu	Ala	Glu	Leu		Ala	GIn	His
		755					760					765			_
Leu	Ser	Glu	Thr	Phe	Asp		<u>Ile</u>	Asp	Asn	Leu		Pro	Lys	Ala	Ser
	770					775					<u>780</u>				_
His	Arg	Ser	Lys	Gln	Arg	His	Lys	Gln	Ser		Tyr	Gly	Asp	Tyr	
785					790					795					800
Phe	Asp	Thr	Asn	Arg	His	Asp	Asp	Asn	Arg	Ser	Asp	Asn	Phe		Thr
				805					810					815	
Gly	Asn	Met	Thr	Val	Leu	Ser	Pro		Leu	Asn	Thr	Thr		Leu	Pro
			820					825					<u>830</u>		

501	Ser		Ser	Ser	Arg	Gly		Leu	Asp	Ser	Ser		Ser	Glu	Lys
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Dwo	850	(III)b as	<u> </u>	7	D	855	m1	a	<u> </u>	T	860	~1	_	~1	
	Ala	1111	GIU	ASII		СТХ	Thr	ser	Ser		Arg	GIY	ьеи	GIn	
865	πh.×	Пhr	772	71-	870	T10	775	T	1701	875	01	01	77-1	<u> </u>	880
ser	Thr	1111	Ата	885	GIII	тте	Ala	ьуs		мес	GIU	GIU	val		Ala
T10	uic	Thr	Cox		C1.,	7 00	7 200	Cox	890	<u> </u>	Con	(T) la sa	ml	895	T
116	His	1111	900	GIII	GIU	ASD	Arg		Ser	GIA	Ser	THE		GIU	Leu
ui c	Cvc	17a 1		7 cn	C1,1	λκα	7 an	905	T 011	7 ~~	7	Com	910	7.1 ~	77-
1115	Cys	915	1111	ASD	Giu	Arg	920	Ala	пеп	Arg	Arg	925	ser	Ата	Ala
His	Thr		Sor	Acn	Thr	Фиг		Dho	Thr	Tara	Cor		7 an	Cox	7 an
1115	930	1113	DCL	ASII	1111	935	ASII	FIIE	1111	цуъ	940	GIU	ASII	Ser	ASII
Arg		Cve	Ser	Mot	Dro		λ1 a	Laze	Lou	G111		Tara	7~~	Ser	802
945	1111	СУЗ	DCT	Hec	950	1 7 1	Ата	шуъ	пец	955	<u> 1 </u>	шуъ	Arg	per	960
	Asp	Ser	Len	Agn		Val	Ser	Ser	Ser		Glv	Пълг	Glaz	Lvc	
11011	1100	DCI	пси	965	DCI	Vai	DCI	Der	970	дор	Сту	<u> </u>	Сту	975	ALG
Glv	Gln	Met	Lvs		Ser	Tle	G111	Ser		Ser	Glu	Agn	Acn		Sor
<u>017</u>	0111	1100	980	110	501		014	985	<u>+ y +</u>	DCI	Gra	тэр	990	GIU	261
Lvs	Phe	Cvs		Tyr	Glv	Gln	Tyr		Δla	Asn	T.eu	Δla		Lvc	Tle
<u> </u>		995	001	<u> </u>	<u> </u>	0211	1000		7114	2150	пси	1005		цуь	116
His	Ser		Asn	His	Met	Asp			Asp	Glv	Glu		_	Thr	Pro
	1010					1015			1122	<u></u>	1020		2100		110
Ile	Asn		Ser	Leu	Lvs			Asp	Glu	Gln		-	Ser	Glv	Ara
102					1030					1035				<u> </u>	1040
Gln	Cor	Dree	~	~ 7											
	Ser	PIO	Ser	GIn	Asn	Glu	Arg	Trp	Ala	Arg	Pro	Lys	His	Ile	Ile
	Ser	PIO	Ser	1045		Glu	Arg	Trp	Ala 1050		Pro	Lys	His	Ile 1055	
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				1045 Lys	5				1050 Arg)				1055 Gln	<u> </u>
Glu		Glu	Ile 1060	1045 Lys)	Gln	Ser	Glu	Gln 1065	1050 Arg) Gln	Ser	Arg	Asn 1070	1055 Gln)	Ser
Glu	Asp	Glu	Ile 1060 Pro	1045 Lys)	Gln	Ser	Glu	Gln 1065 Ser	1050 Arg) Gln	Ser	Arg	Asn 1070 His	1055 Gln)	Ser
Glu	Asp	Glu Tyr 1075	Ile 1060 Pro	1045 Lys) Val	Gln Tyr	Ser Thr	Glu Glu 1080	Gln 1065 Ser	1050 Arg Thr	Gln Asp	Ser	Arg Lys	Asn 1070 His	1055 Gln) Leu	Ser Lys
Glu	Asp Thr	Glu Tyr 1075 Pro	Ile 1060 Pro	1045 Lys) Val	Gln Tyr	Ser Thr	Glu Glu 1080 Gln	Gln 1065 Ser	1050 Arg Thr	Gln Asp	Ser	Arg Lys 1085 Pro	Asn 1070 His	1055 Gln) Leu	Ser Lys
Glu Thr Phe	Asp Thr	Glu Tyr 1075 Pro	Ile 1060 Pro His	1049 Lys Val	Gln Tyr Gly	Ser Thr Gln 1095	Glu Glu 1080 Gln	Gln 1065 Ser Glu	1050 Arg Thr	Gln Asp Val	Ser Asp Ser 1100	Arg Lys 1085 Pro	Asn 1070 His Tyr	1055 Gln Leu Arg	Ser Lys Ser
Glu Thr Phe	Asp Thr Gln 1090 Gly	Glu Tyr 1075 Pro	Ile 1060 Pro His	1049 Lys Val	Gln Tyr Gly	Ser Thr Gln 1095	Glu Glu 1080 Gln	Gln 1065 Ser Glu	1050 Arg Thr	Gln Asp Val	Ser Asp Ser 1100 Gly	Arg Lys 1085 Pro	Asn 1070 His Tyr	1055 Gln Leu Arg	Ser Lys Ser
Glu Thr Phe Arg	Asp Thr Gln 1090 Gly	Glu Tyr 1075 Pro	Ile 1060 Pro His	Lys Val Phe Gly Val	Gln Tyr Gly Ser 1110	Ser Thr Gln 1095 Glu	Glu Glu 1080 Gln Thr	Gln 1065 Ser Glu Asn	Thr Cys Arg	Gln Asp Val Val Gln	Ser Asp Ser 1100 Gly	Lys 1085 Pro	Asn 1070 His Tyr	1055 Gln) Leu Arg	Ser Lys Ser Gly 1120
Glu Thr Phe Arg	Asp Thr Gln 1090 Gly	Glu Tyr 1075 Pro	Ile 1060 Pro His	Lys Val Phe	Gln Tyr Gly Ser 1110	Ser Thr Gln 1095 Glu	Glu Glu 1080 Gln Thr	Gln 1065 Ser Glu Asn	Thr Cys Arg	Gln Asp Val Val Gln	Ser Asp Ser 1100 Gly	Lys 1085 Pro	Asn 1070 His Tyr	1055 Gln) Leu Arg	Ser Lys Ser Gly 1120 Glu
Thr Phe Arg 1105	Asp Thr Gln 1090 Gly	Tyr 1075 Pro Ala	Ile 1060 Pro His Asn	Lys Val Phe Gly Val 1125	Gln Tyr Gly Ser 1110 Ser	Thr Gln 1095 Glu Gln Gln	Glu 1080 Gln Thr	Gln 1065 Ser Glu Asn	Thr Cys Arg Cys 1130	O Gln Asp Val Val Gln Gln O)	Ser Asp Ser 1100 Gly Glu	Lys 1085 Pro Ser	Asn 1070 His Tyr Asn Asp	1055 Gln Leu Arg His	Ser Ser Ser 1120 Glu
Thr Phe Arg 1105	Thr Gln 1090 Gly Asn	Tyr 1075 Pro Ala	Ile 1060 Pro His Asn	Lys Val Phe Gly Val 1125	Gln Tyr Gly Ser 1110 Ser	Thr Gln 1095 Glu Gln Gln	Glu 1080 Gln Thr	Gln 1065 Ser Glu Asn	1050 Arg Thr Cys Arg Cys 1130 Arg	O Gln Asp Val Val Gln Gln O)	Ser Asp Ser 1100 Gly Glu	Lys 1085 Pro Ser Asp	Asn 1070 His Tyr Asn Asp	1055 Gln) Leu Arg His Tyr 1135 Glu	Ser Ser Ser 1120 Glu
Thr Phe Arg 1109	Thr Gln 1090 Gly Asn	Glu Tyr 1075 Pro Ala Gln Lys	Ile 1060 Pro His Asn Asn	Lys Val Phe Gly Val 1125 Thr	Gln Tyr Gly Ser 1110 Ser Asn	Ser Thr Gln 1095 Glu Gln Tyr	Glu Glu 1080 Gln Thr Ser	Gln 1065 Ser Glu Asn Leu Glu 1145	1050 Arg Thr Cys Arg Cys 1130 Arg	Olamon Asp Val Val 1115 Gln Tyr	Ser Asp Ser 1100 Gly Glu Ser	Lys 1085 Pro Ser Asp	Asn 1070 His Tyr Asn Asp	1055 Gln Leu Arg His Tyr 1135 Glu	Ser Lys Ser Gly 1120 Glu Gln
Thr Phe Arg 1109 Ile Asp	Asp Gln 1090 Gly Asn Asp	Glu Tyr 1075 Pro Ala Gln Lys Glu 1155	Ile 1060 Pro His Asn Asn Pro 1140 Glu	Lys) Val Phe Gly Val 1125 Thr) Glu	Gln Tyr Gly Ser 1110 Ser Asn Arg	Ser Thr Gln 1095 Glu Gln Tyr Pro	Glu Glu 1080 Gln Thr Ser Ser Thr	Gln 1065 Ser Glu Asn Leu Glu 1145 Asn	1050 Arg Thr Cys Arg Cys 1130 Arg	Old Carry Ca	Ser Asp Ser 1100 Gly Glu Ser Ile	Lys 1085 Pro Ser Asp Glu Lys 1165	Asn 1070 His Tyr Asn Asp Glu 1150 Tyr	Gln) Leu Arg His Tyr 1135 Glu Asn	Ser Lys Ser Gly 1120 Glu Glu Gln
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Thr Phe Arg 1105 Ile Asp His	Asp Gln 1090 Gly Asn Asp Glu Lys 1170 Asp	Tyr 1075 Pro Ala Gln Lys Glu 1155 Arg	Ile 1060 Pro His Asn Asn Pro 1140 Glu His	Lys Val Phe Gly Val 1125 Thr Clu Val	Gln Tyr Gly Ser 1110 Ser Asn Arg	Ser Thr Gln 1095 Glu Gln Tyr Pro Gln 1175 Gln	Glu Glu 1080 Gln Thr Ser Ser Thr 1160 Pro	Gln 1065 Ser Glu Asn Leu Glu 1145 Asn	Thr Cys Arg Cys 1130 Arg Tyr Asp	Oln Asp Val Val 1115 Gln Tyr Ser Tyr	Ser Asp Ser 1100 Gly Glu Ser Ile Ser 1180 Ser	Lys 1085 Pro Ser Asp Glu Lys 1165 Leu	Asn 1070 His Tyr Asn Asp Glu 1150 Tyr	Gln Leu Arg His Tyr 1135 Glu Asn	Ser Lys Ser Gly 1120 Glu Glu Glu Ala Ser
Thr Phe Arg 1105 Ile Asp His Glu Thr	Asp Gln 1090 Gly Asn Asp Glu Lys 1170 Asp	Tyr 1075 Pro Ala Gln Lys Glu 1155 Arg	Ile 1060 Pro His Asn Pro 1140 Glu His	Lys) Val Phe Gly Val 1125 Thr) Glu Val	Gln Tyr Gly Ser 1110 Ser Asn Arg Asp	Ser Thr Gln 1095 Glu) Gln Tyr Pro Gln 1175 Gln	Glu Glu 1080 Gln Thr Ser Ser Thr 1160 Pro	Gln 1065 Ser Glu Asn Leu Glu 1145 Asn Ile	Thr Cys Arg Cys 1130 Arg Tyr Asp	Older Control	Ser Asp Ser 1100 Gly Glu Ser Ile Ser 1180 Ser	Lys 1085 Pro Ser Asp Glu Lys 1165 Leu Phe	Asn 1070 His Tyr Asn Asp Glu 1150 Tyr Lys Ser	Gln Leu Arg His Tyr 1135 Glu Asn Tyr	Ser Lys Ser Gly 1120 Glu Glu Glu Ala Ser 1200
Thr Phe Arg 1105 Ile Asp His Glu Thr	Asp Gln 1090 Gly Asn Asp Glu Lys 1170 Asp	Tyr 1075 Pro Ala Gln Lys Glu 1155 Arg	Ile 1060 Pro His Asn Pro 1140 Glu His	1045 Lys) Val Phe Gly Val 1125 Thr) Glu Val Ser	Gln Tyr Gly Ser 1110 Ser Asn Arg Asp Ser 1190 Ser	Ser Thr Gln 1095 Glu) Gln Tyr Pro Gln 1175 Gln	Glu Glu 1080 Gln Thr Ser Ser Thr 1160 Pro	Gln 1065 Ser Glu Asn Leu Glu 1145 Asn Ile Gln Glu	Thr Cys Arg Cys 1130 Arg Tyr Asp Ser	Oln Asp Val Val 1115 Gln Tyr Ser Tyr Phe 1195 Met	Ser Asp Ser 1100 Gly Glu Ser Ile Ser 1180 Ser	Lys 1085 Pro Ser Asp Glu Lys 1165 Leu Phe	Asn 1070 His Tyr Asn Asp Glu 1150 Tyr Lys Ser	1055 Gln Leu Arg His Tyr 1135 Glu Asn Tyr Lys Ser	Ser Lys Ser Gly 1120 Glu Glu Ala Ser 1200 Glu
Thr Phe Arg 1105 Ile Asp His Glu Thr 1185	Asp Thr Gln 1090 Gly Asn Asp Glu Lys 1170 Asp Ser	Tyr 1075 Pro Ala Gln Lys Glu 1155 Arg	Ile 1060 Pro His Asn Asn Pro 1140 Glu His Pro Gln	1045 Lys Val Phe Gly Val 1125 Thr Clu Val Ser 1205	Gln Tyr Gly Ser 1110 Ser Asn Arg Asp Ser 1190 Ser	Ser Thr Gln 1095 Glu Gln Tyr Pro Gln 1175 Gln Lys	Glu 1080 Gln Thr Ser Thr 1160 Pro	Gln 1065 Ser Glu Asn Leu Glu 1145 Asn Ile Gln Glu	Thr Cys Arg Cys 1130 Arg Tyr Asp Ser His	Oln Asp Val Val 1115 Gln Tyr Ser Tyr Phe 1195 Met	Ser Asp Ser 1100 Gly Glu Ser Ile Ser 1180 Ser	Lys 1085 Pro Ser Asp Glu Lys 1165 Leu Phe	Asn 1070 His Tyr Asn Asp Glu 1150 Tyr Lys Ser	1055 Gln Leu Arg His Tyr 1135 Glu Asn Tyr Lys Ser 1215	Ser Lys Ser Gly 1120 Glu Glu Ala Ser 1200 Glu
Thr Phe Arg 1105 Ile Asp His Glu Thr 1185	Asp Gln 1090 Gly Asn Asp Glu Lys 1170 Asp	Tyr 1075 Pro Ala Gln Lys Glu 1155 Arg	Ile 1060 Pro His Asn Asn Pro 1140 Glu His Pro Gln Thr	Lys Val Phe Gly Val 1125 Thr O Glu Val Ser 1205 Pro	Gln Tyr Gly Ser 1110 Ser Asn Arg Asp Ser 1190 Ser	Ser Thr Gln 1095 Glu Gln Tyr Pro Gln 1175 Gln Lys	Glu 1080 Gln Thr Ser Thr 1160 Pro	Gln 1065 Ser Glu Asn Leu Glu 1145 Asn Ile Gln Glu Ala	Thr Cys Arg Cys 1130 Arg Tyr Asp Ser His 1210 Lys	Oln Asp Val Val 1115 Gln Tyr Ser Tyr Phe 1195 Met	Ser Asp Ser 1100 Gly Glu Ser Ile Ser 1180 Ser	Lys 1085 Pro Ser Asp Glu Lys 1165 Leu Phe	Asn 1070 His Tyr Asn Asp Glu 1150 Tyr Ser Ser	Oln Leu Arg His Tyr 1135 Glu Asn Tyr Lys Ser 1215 Leu	Ser Lys Ser Gly 1120 Glu Glu Ala Ser 1200 Glu
Thr Phe Arg 1105 Ile Asp His Glu Thr 1185 Ser Asn	Asp Thr Gln 1090 Gly Asn Asp Glu Lys 1170 Asp Ser	Tyr 1075 Pro Ala Gln Lys Glu 1155 Arg Ile Gly Ser	Ile 1060 Pro His Asn Asn Pro 1140 Glu His Pro Gln Thr	Lys Val Phe Gly Val 1125 Thr Clu Val Ser 1205 Pro	Gln Tyr Gly Ser 1110 Ser Asn Arg Asp Ser 1190 Ser	Ser Thr Gln 1095 Glu Gln Tyr Pro Gln 1175 Gln Lys Ser	Glu Glu 1080 Gln Thr Ser Ser Thr Lys Thr Asn	Gln 1065 Ser Glu Asn Leu Glu 1145 Asn Ile Gln Glu Ala 1225	Thr Cys Arg Cys 1130 Arg Tyr Asp Ser His 1210 Lys	Older Color	Ser Asp Ser 1100 Gly Glu Ser 1180 Ser Ser Gln	Lys 1085 Pro Ser Asp Glu Lys 1165 Leu Phe Ser	Asn 1070 His Tyr Asn Asp Glu 1150 Tyr Ser Ser Gln 1230	Arg His Tyr 1135 Glu Asn Tyr Lys Ser 1215	Ser Lys Ser Gly 1120 Glu Glu Ala Ser 1200 Glu His

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1250	Cys Lys Val	Ser Ser	Ile Asr	Gln	Glu Thr	Tle G	ln Thr	í Tvr Cvs	Val
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His Pro Arg Thr Lys Ser Ser Arg Leu Gln Gly Ser Ser Leu Ser Ser Glv Ala Clu Pro Ser Ser Leu Ser Ser Glv Ala Clu Pro Ser Ser Ser Gly Ala Lys Ser Ser Ser Lys Ser Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Lys Gln Gln Glu Thr Pro Lus Ser Arg Cys Thr Ser Val Ser Ser Ser Gly Ala Gln Thr Pro Lys Ser Pro Pro Glu His Tyr Lys Gln Gln Glu Thr Pro Lus Met Pro Ser Arg Cys Thr Ser Val Ser Ser Ser Lys Thr Ser Ser Glu Ala Ser Ser Val Gln Ser Glu Ala Ser Ser Fro Glu Gln Ser Glu Ala Ser Ser Fro Ser Arg Ser Fro Glu Gln Ser Glu Ala Ser Ser Lys Thr Pro Pro Lys Ser Glu Gln Ser Glu Ala Ser Ser Lys Thr Pro Pro Lys Ser Glu Ala Lys Ser Glu Ala Clu Pro Lys Gln Ala Ala Val Gln Glu Ala Clu Pro Lys Gln Ala Ala Val Gln Clu Pro Lys Gln Ala Ala Val Gln Clu Ala Clu Pro Lys Gln Ala Ala Val Gln Clu Ala Clu Ala									GIII
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1345	Glu Ser Ala	Ara Hic	Tyc Ala	V21 C	Tlu Dho	Cor C		712 Trre	Com
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Name		Sor Clu	1330 Cln	Why I	Oro Tira	Cor D	lwo Dwo	Claratic	
Ser Glu Glu Thr Pro Leu Met Pro Ser Arg Cys Thr Ser Val Ser Ser Ser Arg Ser Fle Glu Ser Arg Ser Fle Ala Ser Ser Val Gln Ser Glu Glu Fle Glu Ser Glu Glu Fle Glu Ser Glu Glu Fle Glu Glu	FIO SEL DYS	136	F AIA GIII	. TIIT E	1270				
Table Tabl	Val Cla Clu	TJ0	J Not	Dho C	13/C	Crra III	Ibas Cass	137:	<u>-</u>
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Pro	Tou Nam Com		C 3	<u>1</u>	[] -]] -	G G			~1
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1410				21 -	-1 -1		1405		_
Asp Ser Pro Gly Gln Thr Met Pro Pro Ser Arg Ser Lys Thr Pro Pro 1425								Asp Leu	Pro
1425			141	5		1			
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141 141		~	1430			1435			
Ala Pro Thr Ala Glu Lys Arg Glu Ser Gly Pro Lys Gln Ala Ala Val	Pro Pro Pro								
1460 1465 1470 Asn Ala Ala Val Gln Val Leu Pro Asp Ala Asp Thr Leu Leu His Phe Ala Thr Glu Ser Thr Pro Asp Gly Phe Ser Cys Ser Ser Ser Ser Interest of the color		144	<u> </u>		1450)		1455	
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$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$					1530				
Ala Glu Lys Thr Ile Asp Ser Glu Lys Asp Leu Leu Asp Asp Ser Asp 1555	Thr Glu Ser		Pro Lys			Glu A	sn Gln		Glu
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$									
Asp Asp Ile Glu Ile Leu Glu Glu Cys Ile Ile Ser Ala Met Pro Thr Lys Ser Ser Arg Lys Ala Lys Pro Ala Gln Thr Ala Ser Lys 1585 1590 1595 1600 Leu Pro Pro Val Ala Arg Lys Pro Ser Gln Leu Pro Val Tyr Lys Leu Pro Pro Ser Gln Asn Arg Leu Gln Pro Val Ser Phe Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro			Asp Ser		ys Asp	Leu L			Asp
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$								-	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$		Ile Glu			Slu Cys			Ala Met	Pro
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$									
		Ser Arg		Lys L			<u>ln Thr</u>	Ala Ser	Lys
Leu Leu Pro Ser Gln Asn Arg Leu Gln Pro Gln Lys His Val Ser Phe 1620 1625 1630 Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro	Leu Pro Pro			Lys P	ro Ser	Gln L	eu Pro	Val Tyr	Lys
Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro									-
Thr Pro Gly Asp Asp Met Pro Arg Val Tyr Cys Val Glu Gly Thr Pro	Leu Leu Pro		Asn Arg			Gln L	ys His		Phe
<u>1635</u> 1640 1645			Met Pro		al Tyr	Cys V			Pro
	163	5		1640			1645	•	

Ile Asn Phe Se	Thr				Leu	Ser	Asp	Leu	Thr	Ile	Glu	Ser
1650			1655					1660	_			
Pro Pro Asn Gli	ı Leu	Ala	Ala	Gly	Glu	Gly	Val	Arg	Gly	Gly	Ala	<u>Gln</u>
1665		1670)				1675	5				1680
Ser Gly Glu Pho	e Glu	Lys	Arg	Asp	Thr	Ile	Pro	Thr	Glu	Gly	Arg	Ser
	1685	5				1690)				1695	5
Thr Asp Glu Ala	a Gln	Gly	Gly	Lys	Thr	Ser	Ser	Val	Thr	Ile	Pro	Glu
170	00				1705	5				1710)	
Leu Asp Asp Ası	ı Lys	Ala	Glu	Glu	Gly	Asp	Ile	Leu	Ala	Glu	Cys	Ile
1715				1720)				1725	5		
Asn Ser Ala Me	Pro	Lys	Gly	Lys	Ser	His	Lys	Pro	Phe	Arg	Val	Lys
1730			1735					1740				
Lys Ile Met Asy	Gln	Val	Gln	Gln	Ala	Ser	Ala	Ser	Ser	Ser	Ala	Pro
1745		1750					1755					1760
Asn Lys Asn Gli	ı Leu	Asp	Gly	Lys	Lys	Lys	Lys	Pro	Thr	Ser	Pro	Val
-	1765					1770					1775	
Lys Pro Ile Pro		-	Thr	Glu	Tvr			Ara	Val	Ara	-	_
178					1785					1790		
Ala Asp Ser Lys		Asn	Leu				Ara	Val	Phe		-	Asn
1795			-	1800			<u></u>		1805		<u>_</u>	
Lys Asp Ser Lys	LVS	G1n				Asn	Asn	Ser		_	Phe	Asn
1810	, 1,5		1815					1820		2100		
Asp Lys Leu Pro	λsn				Ara	Va1	Ara		-	Phe	Δla	Phe
1825	Abii	1830		1150	**** 9	<u> </u>	1835		001			1840
Asp Ser Pro His	Hic			Pro	Tle	Glu			Pro	Tyr	Cvs	
ASP DCI IIO III.	1845		1111	110	110	1850			110	<u> </u>	1855	
						100	·					_
Ser Ara Ash Asi	Ser	T.011	Ser	Ser	T.eu	Asn	Phe	Agn	Acn	Asn	Asn	Val
Ser Arg Asn Asp		Leu	Ser	Ser			Phe	Asp	Asp			<u>Val</u>
186	50				1865	5				1870	<u>)</u>	
Asp Leu Ser Arg	50		Ala	Glu	1865 Leu	5			Lys	1870 Glu	<u>)</u>	
Asp Leu Ser Arg 1875	Glu	Lys	Ala	Glu 1880	1865 Leu)	Arg	Lys	Ala	Lys 1885	1870 Glu	Asn	Lys
Asp Leu Ser Arg 1875 Glu Ser Glu Ala	Glu	Lys	Ala Thr	Glu 1880 Ser	1865 Leu)	Arg	Lys	Ala Leu	Lys 1885 Thr	1870 Glu	Asn	Lys
Asp Leu Ser Arg 1875 Glu Ser Glu Ala 1890	o Glu Lys	Lys Val	Ala Thr 1895	Glu 1880 Ser	1865 Leu) His	Arg Thr	Lys Glu	Ala Leu 1900	Lys 1885 Thr	1870 Glu Ser	Asn Asn	Lys Gln
180 1875	o Glu Lys	Lys Val Thr	Ala Thr 1895 Gln	Glu 1880 Ser	1865 Leu) His	Arg Thr	Lys Glu Lys	Ala Leu 1900 Gln	Lys 1885 Thr	1870 Glu Ser	Asn Asn	Lys Gln Arg
Asp Leu Ser Arg	oo g Glu a Lys n Lys	Lys Val Thr	Ala Thr 1895 Gln	Glu 1880 Ser Ala	1865 Leu His	Arg Thr	Lys Glu Lys 1915	Leu 1900 Gln	Lys 1885 Thr Pro	1870 Glu Ser Ile	Asn Asn Asn	Lys Gln Arg 1920
180 1875	of Glu Lys Lys Pro	Lys Val Thr 1910	Ala Thr 1895 Gln	Glu 1880 Ser Ala	1865 Leu His	Arg Thr Ala Gln	Lys Glu Lys 1915	Leu 1900 Gln	Lys 1885 Thr Pro	1870 Glu Ser Ile	Asn Asn Asn Gln	Cln Arg 1920 Ser
Asp Leu Ser Arg	GO Glu Lys Lys Pro 1925	Val Thr 1910	Thr 1895 Gln) Leu	Glu 1880 Ser Ala	1865 Leu) His Ile	Thr Ala Gln 1930	Lys Glu Lys 1915 Ser	Leu 1900 Gln Thr	Lys 1885 Thr) Pro	Ser Ile	Asn Asn Gln 1935	Lys Gln Arg 1920 Ser
180 Asp Leu Ser Arg 1875	GO Glu A Lys Lys Pro 1925	Val Thr 1910 Ile Asp	Thr 1895 Gln) Leu	Glu 1880 Ser S Ala Gln	Lys Ala	Thr Ala Gln 1930 Ala	Lys Glu Lys 1915 Ser)	Leu 1900 Gln Thr	Lys 1885 Thr) Pro	Ser Ile Pro	Asn Asn Gln 1935	Lys Gln Arg 1920 Ser
180 Asp Leu Ser Arg 1875	GO G	Val Thr 1910 Ile Asp	Thr 1895 Gln Leu	Glu 1880 Ser Ala Gln	1865 Leu His Ile Lys Ala	Thr Ala Gln 1930 Ala	Lys Lys 1915 Ser)	Leu 1900 Gln Thr	Lys 1885 Thr) Pro Phe Glu	Ser Ile Pro Lys	Asn Asn Gln 1935 Leu	Gln Arg 1920 Ser Gln
180 Asp Leu Ser Arg 1875	GO G	Val Thr 1910 Ile Asp	Thr 1895 Gln Leu	Glu 1880 Ser Ala Gln Gly	Leu His Lys Ala 1945 Val	Thr Ala Gln 1930 Ala	Lys Lys 1915 Ser)	Leu 1900 Gln Thr	Lys 1885 Thr) Pro Phe Glu	Ser Ile Pro Lys 1950	Asn Asn Gln 1935 Leu	Gln Arg 1920 Ser Gln
180 Asp Leu Ser Arg 1875 Glu Ser Glu Ala 1890 Gln Ser Ala Ass 1905 Gly Gln Pro Lys Ser Lys Asp Ila 1955 Lys Ila 1955 Gly Gln Pro Lys Ila	GO G Glu A Lys Lys G Pro 1925 Pro 40 G Glu	Lys Val Thr 1910 Ile Asp Asn	Thr 1895 Gln) Leu Arg	Glu 1880 Ser Ala Gln Gly Pro	Leu His Lys Ala 1945 Val	Thr Ala Gln 1930 Ala Cys	Lys Glu Lys 1915 Ser) Thr	Leu 1900 Gln Thr Asp	Lys 1885 Thr Pro Phe Glu His 1965	Ser Ile Pro Lys 1950 Asn	Asn Asn Gln 1935 Leu Ser	Gln Arg 1920 Ser Gln Ser
180 Asp Leu Ser Arg 1875 Ser Glu Ala 1890 Gln Ser Ala Asr 1905 Gly Gln Pro Lys Ser Lys Asp Ile 1955 Leu Ser Ser Let Ser Let Ser Let Ser Let Ser Let Ser Let Ser Arg Let Ser Let Ser Arg Let Ser Let Ser Arg Let Ser Arg Let Ser Let Ser Arg Let Ser	GO G Glu A Lys Lys G Pro 1925 Pro 40 G Glu	Lys Val Thr 1910 Ile Asp Asn	Ala Thr 1895 Gln Leu Arg Thr	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp	Leu His Lys Ala 1945 Val	Thr Ala Gln 1930 Ala Cys	Lys Glu Lys 1915 Ser) Thr	Leu 1900 Gln Thr Asp	Lys 1885 Thr) Pro Phe Glu His 1965 Asn	Ser Ile Pro Lys 1950 Asn	Asn Asn Gln 1935 Leu Ser	Gln Arg 1920 Ser Gln Ser
180 Asp Leu Ser Arg 1875 Ser Glu Ala 1890 Gln Ser Ala Asp 1905 Gly Gln Pro Lys Ser Lys Asp Phe Ala Ila 1955 Leu Ser Ser Let 1970 Ser Let 1970 Ser Let 1970 Ser Let 1970 Ser Arg Ar	GO G Glu A Lys Lys Fro 1925 Pro 100 G Glu Ser	Lys Val Thr 1910 Ile Asp Asn Asp	Thr 1895 Gln Leu Arg Thr 11e 1975	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp	Leu His Lys Ala 1945 Val OGln	Arg Thr Ala Gln 1930 Ala Cys Glu	Lys Glu Lys 1915 Ser) Thr Phe	Ala Leu 1900 Gln Thr Asp Ser Asn 1980	Lys 1885 Thr) Pro Phe Glu His 1965 Asn	Ser Ile Pro Lys 1950 Asn Lys	Asn Asn Gln 1935 Leu Ser Glu	Arg 1920 Ser Gln Ser Asn
180 Asp Leu Ser Arg 1875	GO G Glu A Lys Lys Fro 1925 Pro 100 G Glu Ser	Lys Val Thr 1910 Ile Asp Asn Asp	Thr 1895 Gln Leu Arg Thr Ile 1975 Glu	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp	Leu His Lys Ala 1945 Val OGln	Arg Thr Ala Gln 1930 Ala Cys Glu Asp	Lys Glu Lys 1919 Ser Thr Phe Asn	Ala Leu 1900 Gln Thr Asp Ser Asn 1980 Gln	Lys 1885 Thr) Pro Phe Glu His 1965 Asn	Ser Ile Pro Lys 1950 Asn Lys	Asn Asn Gln 1935 Leu Ser Glu	Lys Gln Arg 1920 Ser Gln Ser Asn Ser
180 Asp Leu Ser Arg 1875 Ser Glu Ala 1905 Gly Gln Pro Lys	GO G Glu A Lys Lys G Pro 1925 Pro 100 Glu Ser Glu	Thr 1910 Ile Asp Asn Thr 1990	Thr 1895 Gln Leu Arg Thr Ile 1975 Glu	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp Pro	Leu His Lys Ala 1945 Val Gln Pro	Arg Thr Ala Gln 1930 Ala Cys Glu Asp	Lys Glu Lys 1919 Ser Thr Phe Asn Ser 1999	Ala Leu 1900 Gln Thr Asp Ser Asn 1980 Gln	Lys 1885 Thr) Pro Phe Glu His 1965 Asn) Gly	Ser Ile Pro Lys 1950 Asn Lys Glu	Asn Asn Gln 1935 Leu Ser Glu Pro	Lys Gln Arg 1920 Ser Gln Ser Asn Ser 2000
180 Asp Leu Ser Arg 1875	GO G Glu A Lys Lys S Pro 1925 Pro 40 Glu Ser Glu A Ser	Thr 1910 Ile Asp Asn Asp Thr 1990 Gly	Thr 1895 Gln Leu Arg Thr Ile 1975 Glu	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp Pro	Leu His Lys Ala 1945 Val Gln Pro	Thr Ala Gln 1930 Ala Cys Glu Asp	Lys Glu Lys 1915 Ser Thr Phe Asn Ser 1995	Ala Leu 1900 Gln Thr Asp Ser Asn 1980 Gln	Lys 1885 Thr) Pro Phe Glu His 1965 Asn) Gly	Ser Ile Pro Lys 1950 Asn Lys Glu	Asn Asn Gln 1935 Leu) Ser Glu Pro	Lys Gln Arg 1920 Ser Gln Ser Asn Ser 2000 Asp
180 1875 1875 1875 1875 1870 1875 1890	GO G	Thr 1910 Ile Asp Asn Asp Thr 1990 Gly	Thr 1895 Gln Leu Arg Thr Ile 1975 Glu Tyr	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp Pro Ala	Leu His Lys Ala 1945 Val Coln Pro	Arg Thr Ala Gln 1930 Ala Cys Glu Asp Lys 2010	Lys Glu Lys 1915 Ser) Thr Phe Asn Ser 1995 Ser	Leu 1900 Gln Thr Asp Ser Asn 1980 Gln Gln	Lys 1885 Thr) Pro Phe Glu His 1965 Asn) Gly His	Ser Ile Pro Lys 1950 Asn Lys Glu Val	Asn Asn Gln 1935 Leu Columbia Pro Glu 2015	Lys Gln Arg 1920 Ser Gln Ser Asn Ser 2000 Asp
## Asp Leu Ser Arg ## 1875 ## Glu Ser Glu Ala ## 1890 ## Gln Ser Ala Ass ## 1905 ## Gly Gln Pro Lys ## Ser Lys Asp Ila ## 1955 ## Leu Ser Ser Leu ## 1970 ## Glu Pro Ile Lys ## 1985 ## Lys Pro Gln Ala ## Thr Pro Val Cys	GO G	Thr 1910 Ile Asp Asn Asp Thr 1990 Gly	Thr 1895 Gln Leu Arg Thr Ile 1975 Glu Tyr	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp Pro Ala	1865 Leu) His Ile Lys Ala 1945 Val) Gln Pro Pro	Thr Ala Gln 1930 Ala Cys Glu Asp Lys 2010 Ser	Lys Glu Lys 1915 Ser) Thr Phe Asn Ser 1995 Ser	Leu 1900 Gln Thr Asp Ser Asn 1980 Gln Gln	Lys 1885 Thr) Pro Phe Glu His 1965 Asn) Gly His	Ser Ile Pro Lys 1950 Asn Cluss Cluss Cluss Lys Lys Lys	Asn Asn Gln 1935 Leu Color Glu 2015 Ser	Lys Gln Arg 1920 Ser Gln Ser Asn Ser 2000 Asp
## Asp Leu Ser Arg ## 1875 ## Glu Ser Glu Ald ## 1890 ## Gln Ser Ala Ass ## 1905 ## Gly Gln Pro Lys ## Ser Lys Asp Ile ## 1955 ## Leu Ser Ser Leu ## 1970 ## Glu Pro Ile Lys ## 1985 ## Lys Pro Gln Ald ## Thr Pro Val Cys ## 2000 ## Asp Leu Ser Ser Leu ## 1985 ## Lys Pro Gln Ald ## Cys ## 2000 ## Asp Leu Ser Ser Leu ## 1970 ## Pro Val Cys ## 2000 ## Asp Leu Ser Ser Ser Ser Ser Leu Ser	GO G	Lys Val Thr 1910 Ile Asp Asn Asp Gly Ser	Thr 1895 Gln Leu Arg Thr Ile 1975 Glu Tyr Arg	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp Pro Ala Asn	His Lys Ala 1945 Val Pro Pro Ser 2025	Thr Ala Gln 1930 Ala Cys Glu Asp Lys 2010 Ser	Lys Glu Lys 1915 Ser) Thr Phe Asn Ser 1995 Ser)	Leu 1900 Gln Thr Asp Ser Asn 1980 Gln Phe	Lys 1885 Thr) Pro Phe Glu His 1965 Asn) Gly His	Ser Ile Pro Lys 1950 Asn Cluss Cluss Cluss Cluss Lys Cluss Lys Cluss Cluss Leu 2030	Asn Asn Gln 1935 Leu Ser Glu Pro Glu 2015 Ser	Gln Arg 1920 Ser Gln Ser Asn Ser 2000 Asp
Asp Leu Ser Arg 1875	GO G	Lys Val Thr 1910 Ile Asp Asn Asp Gly Ser	Thr 1895 Gln Leu Arg Thr Ile 1975 Glu Tyr Arg	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp Asn Gln	Leu His Lys Ala 1945 Val Pro Pro Ser 2025 Glu	Thr Ala Gln 1930 Ala Cys Glu Asp Lys 2010 Ser	Lys Glu Lys 1915 Ser) Thr Phe Asn Ser 1995 Ser)	Leu 1900 Gln Thr Asp Ser Asn 1980 Gln Phe	Lys 1885 Thr) Pro Phe Glu His 1965 Asn) Gly His Ser	I870 Glu Ser Ile Pro Lys 1950 Asn C Lys Glu Val Leu 2030 Ala	Asn Asn Gln 1935 Leu Ser Glu Pro Glu 2015 Ser	Gln Arg 1920 Ser Gln Ser Asn Ser 2000 Asp
## Asp Leu Ser Arg ## 1875 ## Glu Ser Glu Ald ## 1890 ## Gln Ser Ala Ass ## 1905 ## Gly Gln Pro Lys ## Ser Lys Asp Ile ## 1955 ## Leu Ser Ser Leu ## 1970 ## Glu Pro Ile Lys ## 1985 ## Lys Pro Gln Ald ## Thr Pro Val Cys ## 2000 ## Asp Leu Ser Ser Leu ## 1985 ## Lys Pro Gln Ald ## Cys ## 2000 ## Asp Leu Ser Ser Leu ## 1970 ## Pro Val Cys ## 2000 ## Asp Leu Ser Ser Ser Ser Ser Leu Ser	GO G Glu A Lys A Lys Fro 1925 Pro 100 G Glu I Ser S Glu A Ser 2005 S Phe 200 A Sp	Thr 1910 Ile Asp Asn Asp Gly Ser Leu	Thr 1895 Gln Leu Arg Thr Ile 1975 Glu Tyr Arg	Glu 1880 Ser Ala Gln Gly Pro 1960 Asp Pro Ala Asn Gln 2040	Leu His Lys Ala 1945 Val Pro Pro Ser 2025 Glu	Thr Ala Gln 1930 Ala Cys Glu Asp Lys 2010 Ser Cys	Lys Glu Lys 1915 Ser) Thr Phe Asn Ser 1995 Ser) Leu Ile	Ala Leu 1900 Gln Thr Asp Ser Asn 1980 Gln Phe Ser	Lys 1885 Thr Pro Phe Glu His 1965 Asn Gly His Ser Ser	Ser Ile Pro Lys 1950 Asn Lys Glu Val Leu 2030 Ala	Asn Asn Gln 1935 Leu Columbia Ser Glu Pro Glu 2015 Ser Met	Lys Gln Arg 1920 Ser Gln Ser Asn Ser 2000 Asp Ile Pro

2	050)				205	5				206	0			
Pro A	rg	Asn	Met	Gly	Gly			Gly	Glu	Asp			Leu	Asp	Leu
2065			_		2070)				2075	5				2080
Lys A	sp	Ile	Gln	Arg	Pro	Asp	Ser	Glu	His	Gly	Leu	Ser	Pro	Asp	Ser
				208	5				2090)				2095	5
Glu A	sn	Phe			Lys	Ala	Ile	Gln	Glu	Gly	Ala	Asn	Ser	Ile	Val
			210	0				2109	5				2110	<u>)</u>	
Ser Se	er	Leu	His	Gln	Ala	Ala	Ala	Ala	Ala	Cys	Leu	Ser	Arg	Gln	Ala
		211	5				2120)				2125	5		
Ser Se	er	Asp	Ser	Asp	Ser	Ile	Leu	Ser	Leu	Lys	Ser	Gly	Ile	Ser	Leu
	130					213					2140	_			
Gly Se	<u>er</u>	Pro	Phe	His			Pro	Asp	Gln			Lys	Pro	Phe	
2145					2150					2155				•	2160
Ser A	sn	Lys	Gly			Ile	Leu	Lys			Glu	Lys	Ser		
	_			2165					2170					2175	_
Glu Th	hr	Lys			Glu	Ser	Glu			Gly	Ile	Lys			Lys
			2180					2185					2190	-	
Lys V	al_			Ser	Leu	Ile			Lys	Val	Arg			Ser	Glu
		219					2200					2205	-		
Ile Se			Gln	Met	Lys			Leu	Gln	Ala			Pro	Ser	Ile
	210					2215					2220	_			
Ser A	rg	Gly	Arg	Thr	Met	Ile	His	Ile	Pro			Arg	Asn	Ser	Ser
2225					2230					2235					2240
Ser Se	er	Thr	Ser			Ser	Lys	Lys	Gly	Pro	Pro	Leu	Lys	Thr	Pro
				2245	-				2250					2255	_
<u>Ala Se</u>	er	Lys			Ser	Glu	Gly			Ala	Thr	Thr			Arg
			2260					2265					2270	_	
Gly A	la			Ser	Val	Lys			Leu	Ser	Pro			Arg	Gln
		2275					2280					2285	-		
Thr Se			Ile	Gly	Gly			Lys	Ala	Pro			Ser	Gly	Ser
	290					2295					2300	_			
Arg As	sp	Ser	Thr	Pro			Pro	Ala	Gln			Leu	Ser	Arg	
2305					2310					2315					2320
Ile G	ln	Ser	Pro			Asn	Ser	Ile			Gly	Arg	Asn		
				2325			~ 1		2330					2335	_
Ser Pi	ro	Pro			Leu	Ser	GIn			Arg	Thr	Ser			Ser
	1		2340				~ 7	2345		-	36 1		2350	-	~
Thr Al	1a			ьуs	Ser	Ser			GIY	Lys	Met			Thr	Ser
	1	2355		35.1		~1	2360			ml.		2365	-	~ 1	_
Pro G			Gin	Met	Ser			Asn	Leu	Thr			Thr	GLY	Leu
	370			~	~	2375		_	~	~3	2380	_	_	_	~ 3
Ser Ly	ys	Asn	Ala	Ser			Pro	Arg	Ser			Ala	Ser	гля	
2385		<u> </u>	36-1-	-	2390			<u> </u>	. 7	2395		-		01	2400
Leu As	sn	GIn	Met			GIY	Asn	Gly			ьуs	Lys	Val		
				2405				~	2410		~ -			2415	-
Ser A	rg	Met			Thr	Lys	Ser			Ser	Glu	Ser			Ser
			2420				~1	2425					2430	-	
Glu Ai	rg			ьeu	val	arg			Thr	rne	тте			АТА	Pro
<u> </u>		2435		7	7	T	2440		Q1	0	7 7	2445	-	01	0
Ser Pr			Leu	Arg	Arg			GIU	GLU	ser			Pne	GLU	ser
24	450	-				2455)				2460	<u>,</u>			

Leu	Ser	Pro	Ser	Ser	Ara	Pro	Ala	Ser	Pro	Thr	Arg	Ser	Gln	Ala	Gln
2465					2470					2475					2480
		Val	Leu	Ser	Pro	Ser	Leu	Pro	Asp	Met	Ser	Leu	Ser	Thr	His
				2485					2490					249	
Ser	Ser	Val	Gln	Ala	Gly	Gly	Trp	Arg	Lys	Leu	Pro	Pro	Asn	Leu	Ser
			2500					2505					2510		
Pro	Thr	Ile	Glu	Tyr	Asn	Asp	Gly	Arg	Pro	Ala	Lys	Arg	His	Asp	Ile
		2515					2520					2525			
Ala	Arg	Ser	His	Ser	Glu	Ser	Pro	Ser	Arg	Leu	Pro	Ile	Asn	Arg	Ser
	2530					2535					2540				
Gly	Thr	Trp	Lys	Arg	Glu	His	Ser	Lys	His	Ser	Ser	Ser	Leu	Pro	Arg
2545					2550					2555					2560
Val	Ser	Thr	Trp	Arg	Arg	Thr	Gly	Ser	Ser	Ser	Ser	Ile	Leu	Ser	Ala
<u>,</u>				2565					2570					257	
Ser	Ser	Glu	Ser			Lys	Ala	Lys	Ser	Glu	Asp	Glu	Lys	His	Val
202			2580					2585					2590)	
Asn	Ser	Ile	Ser		Thr	Lys	Gln	Ser	Lys	Glu	Asn	Gln	Val	Ser	Al <u>a</u>
		259					2600					260			
LVS	Glv		Trp	Ara	Lvs	Ile			Asn	Glu	Phe	Ser	Pro	Thr	Asn
<u> </u>	2610		1-1	3		261					2620				
Ser	Thr	Ser	Gln	Thr	Val			Glv	Ala	Thr	Asn	Gly	Ala	Glu	Ser
262		DCI	0111		2630					263					2640
Twe	Thr	T.011	Ile	Tyr			Ala	Pro	Ala			Lvs	Thr	Glu	Asp
пуъ	1111	пси	110	264		1100			265					265	_ 5
1721	Trn	Val	Arg			Asn	Cvs	Pro			Asn	Pro	Arq	Ser	Gly
Val	110	Val	2660			1100		2665					267		
Ara	Ser	Pro	Thr		Asn	Thr	Pro			Ile	Asp	Ser	Val	- Ser	Glu
Arg	DCT	267			11011		2680					268			
Lare	Δla		Pro	Asn	Tle	Lvs			Lvs	Asp	Asn	Gln	- Ala	Lys	Gln
шуз	269		110	21011		269					270	0			
Acn	7/2 l	Glv	Asn	Glv	Ser			Met	Ara	Thr			Leu	Glu	Asn
270		GIY	HSII	OIY	271			1100	<u> J</u>	271					2720
270	J. E.D.	Δen	Ser	Phe			Val	Asp	Ala			Gln	Lys	Gly	Thr
Arg	пси	71011	DOL	272					273					273	
<u> </u>	T10	Lare	Pro			Δsn	Asn	Pro			Val	Ser	Glu	Thr	_ Asn
<u> </u>	110	шуз	274		0.2.11	21011	11011	274					275		
Glu	Sar	Ser	Ile		G111	Ara	Thr			Ser	Ser	Ser	Ser	_ Ser	Ser
Giu	Der	275	_		014	1119	276	0			-	276	 5		
Lvc	иiс	Car	Ser	Dro	Ser	Glv	Thr	Va1	Ala	Ala	Ara			Pro	Phe
цуѕ	277		Ser	110	DCI	277					278				
7 00	Tarr	Λcn	Dro	Sor	Dro			Ser	Ser	Ala		_	Thr	Ser	Ala
278		VDII	FIO	DET	279		تا پرند_	204	~	279					2800
2/0	Dro	Cor	Cln	Tlo			Pro	Va1	Asn			Thr	Lvs	Lvs	Arg
MI G	FIO	261	GIII	280					281					281	
7 ~~	Go~	Larc	Thr			Thr	Glu	Ser			Thr	Gln	Ser		Lys
ASD	ser	пув	282		SET	- 1111	<u> </u>	282					283		
7~~	u i c	50~	Gly		Тугт	T.011	Va1			Val				_	
ALG	птв	283		Ser	+ 7 1	700	284		201						
		203	<u> </u>					<u> </u>							

⁽²⁾ INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 31 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (vii) IMMEDIATE SOURCE: (B) CLONE: ral2(yeast) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8: Leu Thr Gly Ala Lys Gly Leu Gln Leu Arg Ala Leu Arg Arg Ile Ala Arg Ile Glu Gln Gly Gly Thr Ala Ile Ser Pro Thr Ser Pro Leu 25 (2) INFORMATION FOR SEQ ID NO:9: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 29 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens (vii) IMMEDIATE SOURCE: (B) CLONE: m3 (mAChR) (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9: Leu Tyr Trp Arg Ile Tyr Lys Glu Thr Glu Lys Arg Thr Lys Glu Leu 5 Ala Gly Leu Gln Ala Ser Gly Thr Glu Ala Glu Thr Glu 25 20 (2) INFORMATION FOR SEQ ID NO:10: (i) SEQUENCE CHARACTERISTICS:

	(A) LENGTH: 29 amino acids(B) TYPE: amino acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: peptide	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(vii)	IMMEDIATE SOURCE: (B) CLONE: MCC	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:10:	
Leu 1	Tyr Pro Asn Leu Ala Glu Glu Arg Ser Arg Trp Glu Lys Glu Leu 5 10 15	
Ala	Gly Leu Arg Glu Glu Asn Glu Ser Leu Thr Ala Met 20 25	
	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:11:	
GTATCAAG	GAC TGTGACTTTT AATTGTAGTT TATCCATTTT	40
(2) INFO	DRMATION FOR SEQ ID NO:12:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:	
TTT	AGAATTT CATGTTAATA TATTGTGTTC TTTTTAACAG	40
(2)	INFORMATION FOR SEQ ID NO:13:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:	
GTA	GATTTTA AAAAGGTGTT TTAAAATAAT TTTTTAAGCT	40
(2)	INFORMATION FOR SEQ ID NO:14:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:	
AAG	CAATTGT TGTATAAAAA CTTGTTTCTA TTTTATTTAG	40
(2)	INFORMATION FOR SEQ ID NO:15:	
	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:	
GTAACTTTTC TTCATATAGT AAACATTGCC TTGTGTACTC	10
(2) INFORMATION FOR SEQ ID NO:16:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:	40
NNNNNNNN NNNGTCCCTT TTTTTAAAAA AAAAAAATAG	
(2) INFORMATION FOR SEQ ID NO:17:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:	
GTAAGTAACT TGGCAGTACA ACTTATTTGA AACTTTAATA	40
(2) INFORMATION FOR SEQ ID NO:18:	

(A) LENGTH: 40 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:	
ATACAAGATA TTGATACTTT TTTATTATTT GTGGTTTTAG	40
(2) INFORMATION FOR SEQ ID NO:19:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:	
GTAAGTTACT TGTTTCTAAG TGATAAAACA GYGAAGAGCT	40
(2) INFORMATION FOR SEQ ID NO:20:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:	
እአመእአአአአርን መእእርመእስመነት ርርመጥጥርጥጥርጥ ጥጥባትጥጥብG	40

(i) SEQUENCE CHARACTERISTICS:

AATAAAACA TAACTAATTA GGTTTCTTGT TTTATTTTAG

	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:21:	
GTTA	.GTAA	AT TSCCTTTTTT GTTTGTGGGT ATAAAAATAG	40
(2)	INFO	RMATION FOR SEQ ID NO:22:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:22:	
ACCA	TTTT	TG CATGTACTGA TGTTAACTCC ATCTTAACAG	40
(2)	INFO	RMATION FOR SEQ ID NO:23:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	

(2) INFORMATION FOR SEQ ID NO:21:

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:	
GTA	ATAAAT TATTTTATCA TATTTTTAA AATTATTTAA	40
(2)	INFORMATION FOR SEQ ID NO:24:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 64 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:	
CATO	ATGTTA TCTGTATTTA CCTATAGTCT AAATTATACC ATCTATAATG TGCTTAATTT	60
TTAC		64
(2)	INFORMATION FOR SEQ ID NO:25:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:	
GTA	CAGAAG ATTACAAACC CTGGTCACTA ATGCCATGAC TACTTTGCTA AG	52
(2)	INFORMATION FOR SEQ ID NO:26:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 46 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	

(A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:	
GGATATTAAA GTCGTAATTT TGTTTCTAAA CTCATTTGGC CCACAG	46
(2) INFORMATION FOR SEQ ID NO:27:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:	
GTATGTTCTC TATAGTGTAC ATCGTAGTGC ATGTTTCAAA	40
(2) INFORMATION FOR SEQ ID NO:28:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 56 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:	
CATCATTGCT CTTCAAATAA CAAAGCATTA TGGTTTATGT TGATTTTATT TTTCAG	56
(2) INFORMATION FOR SEQ ID NO:29:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 43 base pairs(B) TYPE: nucleic acid	

(vi) ORIGINAL SOURCE:

(C) STRANDEDNESS: single

	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:	
GTAA	GACAAA AATGTTTTTT AATGACATAG ACAATTACTG GTG	43
(2)	INFORMATION FOR SEQ ID NO:30:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:	
TTAC	ATGATT GTCTTTTCC TCTTGCCCTT TTTAAATTAG	40
(2)	INFORMATION FOR SEQ ID NO:31:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 44 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:	
GTA	CTTTTT ATAACATGTA TTTCTTAAGA TAGCTCAGGT ATGA	44
(2)	INFORMATION FOR SEQ ID NO:32:	
	(i) SEQUENCE CHARACTERISTICS:	

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

		(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:32:	
GCTT	GGCT	TC AAGTTGNCTT TTTAATGATC CTCTATTCTG TATTTAATTT ACAG	54
(2)	INFO	RMATION FOR SEQ ID NO:33:	
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 65 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:33:	
GTAC	TATT!	TA GAATTTCACC TGTTTTTCTT TTTTCTCTTT TTCTTTGAGG CAGGGTCTCA	60
СТСТ	'G		65
(2)	INFO	RMATION FOR SEQ ID NO:34:	
		SEQUENCE CHARACTERISTICS: (A) LENGTH: 52 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:34:	

(A) LENGTH: 54 base pairs

GCAACTAGTA TGATTTTATG TATAAATTAA TCTAAAATTG ATTAATTTCC AG	52
(2) INFORMATION FOR SEQ ID NO:35:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 42 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:	
GTACCTTTGA AAACATTTAG TACTATAATA TGAATTTCAT GT	42
(2) INFORMATION FOR SEQ ID NO:36:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 40 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:	
CCAACTCNAA TTAGATGACC CATATTCAGA AACTTACTAG	40
(2) INFORMATION FOR SEQ ID NO:37:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 54 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	

(A) ORGANISM: Homo sapiens

(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:37:	
GTATATATA	G AGTTTTATAT TACTTTTAAA GTACAGAATT CATACTCTCA AAAA	54
(2) INFOR	MATION FOR SEQ ID NO:38:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 41 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:38:	
ATTGTGACC	T TAATTTTGTG ATCTCTTGAT TTTTATTTCA G	41
(2) INFOR	RMATION FOR SEQ ID NO:39:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:39:	
TCCCCGCCT	TG CCGCTCTC	18
(2) INFO	RMATION FOR SEQ ID NO:40:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 18 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA

	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:	
GCAG	GCGGCGG CTCCCGTG	18
(2)	INFORMATION FOR SEQ ID NO:41:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:	
GTG	AACGGCT CTCATGCTGC	20
(2)	INFORMATION FOR SEQ ID NO:42:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:	
ACG	TGCGGGG AGGAATGGA	19
(2)	INFORMATION FOR SEQ ID NO:43:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

	(ii) MOLECULE TYPE: cDNA	
	() OPICINAL COIDCE.	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(A) ORDANIDIT. HOMO BAPTONE	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:	
ATGA	TATCTT ACCAAATGAT ATAC	24
(2)	INFORMATION FOR SEQ ID NO:44:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:	
TTAT	TCCTAC TTCTTCTATA CAG	23
(2)	INFORMATION FOR SEQ ID NO:45:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 21 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(b) forologi. Timear	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:	
	(AL) DINORITITON, DIX ID NO	
TACC	CCATGCT GGCTCTTTTT C	21
(2)	INFORMATION FOR SEQ ID NO:46:	
	(i) SEQUENCE CHARACTERISTICS:	

(D) TOPOLOGY: linear

	(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
((vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
((xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:	
TGGGG	SCCATC TTGTTCCTGA	20
(2) I	INFORMATION FOR SEQ ID NO:47:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
((ii) MOLECULE TYPE: cDNA	
((vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
,	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:	
ACAT	TAGGCA CAAAGCTTGC AA	22
(2)	INFORMATION FOR SEQ ID NO:48:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:	
ATCA	AGCTCC AGTAAGAAGG TA	22

	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 19 base pairs	
		(B) TYPE: nucleic acid (C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
		(b) Torollogi. Timedi	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE:	
	, . – ,	(A) ORGANISM: Homo sapiens	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:49:	
			19
TGCC	GCTC	CT GGGTTGTTG	
(2)	TATEO	RMATION FOR SEQ ID NO:50:	
(2)	INFO	RMAIION FOR BEQ ID NO.30.	
	(i)	SEQUENCE CHARACTERISTICS:	
	(-/	(A) LENGTH: 20 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	/ \	ORIGINAL SOURCE:	
	(VI)	(A) ORGANISM: Homo sapiens	
		(11) 01.01212511 1103110 1111	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:50:	
			20
GCC	CCTTC	CT TTCTGAGGAC	20
(2)	INFC	RMATION FOR SEQ ID NO:51:	
	/÷ \	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 21 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: Homo sapiens	
	124) SEQUENCE DESCRIPTION: SEQ ID NO:51:	
	(XI) DEQUEROE BESTELLES .	

(2) INFORMATION FOR SEQ ID NO:49:

TTTTCTCCTG CCTCTTACTG C	21
(2) INFORMATION FOR SEQ ID NO:52:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:	
ATGACACCCC CCATTCCCTC	20
(2) INFORMATION FOR SEQ ID NO:53:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:	
CCACTTAAAG CACATATATT TAGT	24
(2) INFORMATION FOR SEQ ID NO:54:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Homo sapiens

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:		
GTAT	GTATGGAAAA TAGTGAAGAA CC		
(2)	INFORMATION FOR SEQ ID NO:55:		
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
	(ii) MOLECULE TYPE: cDNA		
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:		
TTCT	TAAGTC CTGTTTTCT TTTG	24	
(2)	INFORMATION FOR SEQ ID NO:56:		
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
	(ii) MOLECULE TYPE: cDNA		
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens		
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:		
TTT	AGAACCT TTTTTGTGTT GTG	23	
(2)	INFORMATION FOR SEQ ID NO:57:		
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		

(ii) MOLECULE TYPE: cDNA

	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens		
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:57:		
CTC	CTCAGATTAT ACACTAAGCC TAAC 24			
(2)	INFOR	RMATION FOR SEQ ID NO:58:		
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
	(ii)	MOLECULE TYPE: cDNA		
	(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens		
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:58:		
CAT	GTCTC'	IT ACAGTAGTAC CA	22	
(2)	INFO	RMATION FOR SEQ ID NO:59:		
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
	(ii)	MOLECULE TYPE: cDNA		
		ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens		
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:59:		
AGG	TCCAA	GG GTAGCCAAGG	20	
(2)	INFO	RMATION FOR SEQ ID NO:60:		
	(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 27 base pairs (B) TYPE: nucleic acid		

(C) STRANDEDNESS: single

	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: Homo sapiens	
	· · · · · · · · · · · · · · · · · · ·	
	CRO TR NO CO	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:	
ТААА	AAATGGA TAAACTACAA TTAAAAG	27
(2)	INFORMATION FOR SEQ ID NO:61:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 24 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(II) MODECODE IIFE. CONA	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:	
	(XI) BEQUENCE BESCRIFTION. BEQ IS NOT US	
AAAT	TACAGAA TCATGTCTTG AAGT	24
	THE TOTAL TOP GEO TO NO. (2)	
(2)	INFORMATION FOR SEQ ID NO:62:	
	(i) SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(II) MODECODE IIFE. CDNA	
	(vi) ORIGINAL SOURCE:	
	(A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:	
	(XI) SECOUNCE DESCRIPTION. SEC ID MO.05.	
ACA	CCTAAAG ATGACAATTT GAG	23
(2)	INFORMATION FOR SEQ ID NO:63:	

(D) TOPOLOGY: linear

(i) SEQUENCE CHARACTERISTICS:

	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii) 1	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE:	
	(A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:63:	
TAACTTAGA	T AGCAGTAATT TCCC	24
(2) INFOR	MATION FOR SEQ ID NO:64:	
(i)	SEQUENCE CHARACTERISTICS:	
	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single (D) TOPOLOGY: linear	
	(b) Toronodi. 11medi	
(ii)	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE:	
(,	(A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:64:	
		23
ACAATAAAC	CT GGAGTACACA AGG	23
(2) INFOR	RMATION FOR SEQ ID NO:65:	
(i)	SEQUENCE CHARACTERISTICS:	
(-)	(A) LENGTH: 23 base pairs	
	(B) TYPE: nucleic acid	
	(C) STRANDEDNESS: single	
	(D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE:	
. ,	(A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:65:	
		23
ATAGGTCA	TT GCTTCTTGCT GAT	2,5

(A) LENGTH: 24 base pairs

	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 24 base pairs (B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(i \	ORIGINAL SOURCE:	
	(\(\nu \)	(A) ORGANISM: Homo sapiens	
		(II) Character name baptons	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:66:	
			2.4
TGAA	TTTT	AA TGGATTACCT AGGT	24
(2)	INFO	RMATION FOR SEQ ID NO:67:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 25 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(vi)	ORIGINAL SOURCE:	
		(A) ORGANISM: Homo sapiens	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:67:	
CTTT	TTTT	GC TTTTACTGAT TAACG	25
(2)	INFO.	RMATION FOR SEQ ID NO:68:	
	(i)	SEQUENCE CHARACTERISTICS:	
		(A) LENGTH: 27 base pairs	
		(B) TYPE: nucleic acid	
		(C) STRANDEDNESS: single	
		(D) TOPOLOGY: linear	
	(ii)	MOLECULE TYPE: cDNA	
	(374)	ORIGINAL SOURCE:	
	(AT)	(A) ORGANISM: Homo sapiens	
		(,	
	(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:68:	
	• '		

(2) INFORMATION FOR SEQ ID NO:66:

TGTAATTCAT TTTATTCCTA ATA[G]CCTC	27
(2) INFORMATION FOR SEQ ID NO:69:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:	
GGTAGCCATA GTATGATTAT TTCT	24
(2) INFORMATION FOR SEQ ID NO:70:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:	
CTACCTATTT TTATACCCAC AAAC	24
(2) INFORMATION FOR SEQ ID NO:71:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA 	
(II) MODECOLE IIII. COMA	

(vi) ORIGINAL SOURCE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:	
AAGAAAGCCT ACACCATTTT TGC	23
(2) INFORMATION FOR SEQ ID NO:72:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:	
GATCATTCTT AGAACCATCT TGC	23
(2) INFORMATION FOR SEQ ID NO:73:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:	
ACCTATAGTC TAAATTATAC CATC	24
(2) INFORMATION FOR SEQ ID NO:74:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 20 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single	

(A) ORGANISM: Homo sapiens

(D) TOPOLOGY: linear

	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:	
GTC	TGGCAT TAGTGACCAG	20
(2)	INFORMATION FOR SEQ ID NO:75:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:	
AGTO	GTAATT TTGTTTCTAA ACTC	24
(2)	INFORMATION FOR SEQ ID NO:76:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:	
TGA	GGACTC GGATTTCAC[G]C C	21
(2)	INFORMATION FOR SEQ ID NO:77:	
	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs	

(ii) MOLECULE TYPE: cDNA

(B) TYPE: nucleic acid

	(D) TOPOLOGY: Tinear	
((ii) MOLECULE TYPE: cDNA	
((vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
((xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:	
TCATT	CACTC ACAGCCTGAT GAC	23
(2) I	INFORMATION FOR SEQ ID NO:78:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
((ii) MOLECULE TYPE: cDNA	
((vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
((xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:	
GCTTT	TGAAAC ATGCACTACG AT	22
(2) I	INFORMATION FOR SEQ ID NO:79:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
((ii) MOLECULE TYPE: cDNA	
((vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
((xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:	
AAACA	ATCATT GCTCTTCAAA TAAC	24

(C) STRANDEDNESS: single

(2) INFORMATION FOR SEQ ID NO:80:

(A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:	
TACCATGATT TAAAAATCCA CCAG	24
(2) INFORMATION FOR SEQ ID NO:81:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:	0.0
GATGATTGTC TTTTTCCTCT TGC	23
(2) INFORMATION FOR SEQ ID NO:82:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:	
CTGAGCTATC TTAAGAAATA CATG	24

(i) SEQUENCE CHARACTERISTICS:

(1)	(A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:83:	
TTTTAAAT	GA TCCTCTATTC TGTAT	25
(2) INFO	RMATION FOR SEQ ID NO:84:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:84:	
ACAGAGTC	AG ACCCTGCCTC AAAG	24
(2) INFO	RMATION FOR SEQ ID NO:85:	
(i)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii)	MOLECULE TYPE: cDNA	
(vi)	ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	

(2) INFORMATION FOR SEQ ID NO:83:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:	
TTTCTATTCT TACTGCTAGC ATT	23
(2) INFORMATION FOR SEQ ID NO:86:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:	
ATACACAGGT AAGAAATTAG GA	22
(2) INFORMATION FOR SEQ ID NO:87:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:	
TAGATGACCC ATATTCTGTT TC	22
(2) INFORMATION FOR SEQ ID NO:88:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	

(vi) ORIGINAL SOURCE:

	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:	
CAAT	TAGGTC TTTTTGAGAG TA	22
(2)	INFORMATION FOR SEQ ID NO:89:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:	
GTTA	CTGCAT ACACATTGTG AC	22
(2)	INFORMATION FOR SEQ ID NO:90:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 23 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:	
GCTT	TTTGTT TCCTAACATG AAG	23
(2)	INFORMATION FOR SEQ ID NO:91:	
	 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	

(A) ORGANISM: Homo sapiens

	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:	
TCTC	CCCACAG GTAATACTCC C	21
(2)	INFORMATION FOR SEQ ID NO:92:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 21 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:	
GCTA	AGAACTG AATGGGGTAC G	21
(2)	INFORMATION FOR SEQ ID NO:93:	
	(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 22 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
	(ii) MOLECULE TYPE: cDNA	
	(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:	
CAGO	GACAAAA TAATCCTGTC CC	22
(2)	INFORMATION FOR SEQ ID NO:94:	
	(i) SEQUENCE CHARACTERISTICS:	

(A) LENGTH: 24 base pairs(B) TYPE: nucleic acid

(D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:		
ATTTTCTTAG TTTCATTCTT CCTC		24
(2) INFORMATION FOR SEQ ID NO:95:		
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear		
(ii) MOLECULE TYPE: cDNA		
<pre>(vi) ORIGINAL SOURCE: (A) ORGANISM: Homo sapiens</pre>		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:		
AGAAGGATCCCTTGTGCAGTGTGGA	24	
(2) INFORMATION FOR SEQ ID NO:96:		
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 		
(ii) MOLECULE TYPE: cDNA		
(vi) ORIGINAL SOURCE: (A) Homo sapiens		
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:96		
GACAGGATCCTGAAGCTGAGTTTG	24	
(2) INFORMATION FOR SEQ ID NO:97:		

(C) STRANDEDNESS: single

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 18 base pairs

(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:	
TCAGAAAGTGCTGAAGAG	18
(2) INFORMATION FOR SEQ ID NO:98:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
<pre>(vi) ORIGINAL SOURCE: (A) Homo sapiens</pre>	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:	
GGAATAATTAGGTCTCCAA	19
(2) INFORMATION FOR SEQ ID NO:99:	
 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:	
GCAAATCCTAAGAGAGAACAA	21
(2) INFORMATION FOR SEQ ID NO:100:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs	

(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vi) ORIGINAL SOURCE:

(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:	
GATGGCAAGCTTGAGCCAG	19
(2) INFORMATION FOR SEQ ID NO:101:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:	
GTTCCAGCAGTGTCACAG	18
(2) INFORMATION FOR SEQ ID NO:102:	
(i) SEQUENCE CHARACTERISTICS:(A) LENGTH: 18 base pairs(B) TYPE: nucleic acid(C) STRANDEDNESS: single(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:	
GGGAGATTTCGCTCCTGA	102
(2) INFORMATION FOR SEQ ID NO:103:	
(i) SEOUENCE CHARACTERISTICS:	

(B) TYPE: nucleic acid

(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:103:	
AGTACAAGGA TGCCAATATT ATG	23
(2) INFORMATION FOR SEO ID NO:104:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:104:	
ACTTCTATCT TTTTCAGAAC GAG	23
(2) INFORMATION FOR SEO ID NO:105:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:105:	
ATTTGAATAC TACAGTGTTA CCC	23
(2) INFORMATION FOR SEQ ID NO:106:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 24 base pairs	

(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
•	
(xi) SEOUENCE DESCRIPTION: SEO ID NO:106:	
CTTGTATTCT AATTTGGCAT AAGG	24
(2) INFORMATION FOR SEQ ID NO:107:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	•
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEOUENCE DESCRIPTION: SEO ID NO:107:	
CTGCCCATAC ACATTCAAAC AC	22
(2) INFORMATION FOR SEO ID NO:108:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(11) 110110011 1111 01111	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(14) Alexie Bubiles	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:	
(AL) DECORAGE BEDCEVER FLOW.	
TGTTTGCGTC TTGCCCATCT T	21
(2) INFORMATION FOR SEQ ID NO:109:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 24 base pairs	
(B) TYPE: nucleic acid	

(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi)_ORIGINAL_SOURCE:	
(A) Homo sapiens	
(12) AND SOME DEAD	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:109:	
AGTCTTAAAT ATTCAGATGA GCAG	24
(2) INFORMATION FOR SEQ ID NO:110:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 26 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEOUENCE DESCRIPTION: SEO ID NO:110:	
GTTTCTCTTC ATTATATTTT ATGCTA	26
(2) INFORMATION FOR SEQ ID NO:111:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:111:	
AAGCCTACCA ATTATAGTGA ACG	23
(2) INFORMATION FOR SEO ID NO:112:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	

(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:112:	
AGCTGATGAC AAAGATGATA ATC	23
(2) INFORMATION FOR SEO ID NO:113:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:113:	
AAGAAACAAT ACAGACTTAT TGTG	24
(2) INFORMATION FOR SEO ID NO:114:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:	
ATGAGTGGGG TCTCCTGAAC	20
(2) INFORMATION FOR SEQ ID NO:115:	
(i) SEOUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single	

(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:115:	
ATCTCCCTCC AAAAGTGGTG C	21
(2) INFORMATION FOR SEO ID NO:116:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEOUENCE DESCRIPTION: SEO ID NO:116:	
TCCATCTGGA GTACTTTCTG TG	22
(2) INFORMATION FOR SEO ID NO:117:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:117:	
AGTAAATGCT GCAGTTCAGA GG	22
(2) INFORMATION FOR SEQ ID NO:118:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 19 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	

(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:118:	
CCGTGGCATA TCATCCCCC	19
(2) INFORMATION FOR SEO ID NO:119:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:119:	
CCCAGACTGC TTCAAAATTA CC	22
(2) INFORMATION FOR SEQ ID NO:120:	
(;) CECUENCE CUADACMEDICATOS.	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(i) ODICINAL COURGE	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:120:	
GAGCCTCATC TGTACTTCTG C	21
(2) INFORMATION FOR SEO ID NO:121:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECIUE TYPE: CDNA	

(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:	
CCCTCCAAAT GAGTTAGCTG C	21
(2) INFORMATION FOR SEQ ID NO:122:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:	
TTGTGGTATA GGTTTTACTG GTG	23
(2) INFORMATION FOR SEO ID NO:123:	
127 INFORMATION FOR DEG ID NO.123.	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 23 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:123:	
1317 5202102 2200111 12011 220 15 110.125.	
ACCCAACAAA AATCAGTTAG ATG	23
(2) INFORMATION FOR SEQ ID NO:124:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
12/ 101 011001 : 1111001	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	

(A) Homo sapiens	
(xi) SEOUENCE DESCRIPTION: SEO ID NO:124:	
GTGGCTGGTA ACTTTAGCCT C	21
(2) INFORMATION FOR SEQ ID NO:125:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	•
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:125:	
ATGATGTTGA CCTTTCCAGG G	21
(2) INFORMATION FOR SEQ ID NO:126:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:	
ATTGTGTAAC TTTTCATCAG TTGC	24
(2) INFORMATION FOR SEO ID NO:127:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	

(xi) SEQUENCE DESCRIPTION: SEO ID NO:127:	
AAAGACATAC CAGACAGAGG G	21
(2) INFORMATION FOR SEO ID NO:128:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:	
CTTTTTTGGC ATTGCGGAGC T	21
(2) INFORMATION FOR SEQ ID NO:129:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:129:	
AAGATGACCT GTTGCAGGAA TG	22
(2) INFORMATION FOR SEQ ID NO:130:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 24 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	

(xi) SEQUENCE DESCRIPTION: SEO ID NO:130:	
GAATCAGACC AAGCTTGTCT AGAT	24
(2) INFORMATION FOR SEQ ID NO:131:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 24 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:131:	
CAATAGTAAG TAGTTTACAT CAAG	24
(2) INFORMATION FOR SEO ID NO:132:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:	
AAACAGGACT TGTACTGTAG GA	22
(2) INFORMATION FOR SEO ID NO:133:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 21 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(vi) SECTIENCE DESCRIPTION: SECTION NO:133:	

CAGCCCCTTC AAGCAAACAT C	
(2) INFORMATION FOR SEO ID NO:134:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(b) Toronogi: Timeat	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:134:	
GAGGACTTAT TCCATTTCTA CC	22
(2) INFORMATION FOR SEQ ID NO:135:	
(i) SEOUENCE CHARACTERISTICS:	
(A) LENGTH: 20 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
(A) NOMO SAPICIIS	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:	
CAGTCTCCTG GCCGAAACTC	20
(2) INFORMATION FOR SEO ID NO:136:	
(i) SEQUENCE CHARACTERISTICS:	
(A) LENGTH: 22 base pairs	
(B) TYPE: nucleic acid	
(C) STRANDEDNESS: single	
(D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE:	
(A) Homo sapiens	
/A/ HOMO SAPTEMS	
(vi) SECTIFNCE DESCRIPTION, SEC ID NO.136.	

GTTGACTGGC GTACTAATAC AG	22
(2) INFORMATION FOR SEO ID NO:137:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 23 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:137:	
TGGTAATGGA GCCAATAAAA AGG	23
(2) INFORMATION FOR SEO ID NO:138:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 20 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:	
TGGGACTTTT CGCCATCCAC	20
(2) INFORMATION FOR SEQ ID NO:139:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:139:	
TGTCTCTATC CACACATTCG TC	22

(2) INFORMATION FOR SEQ ID NO:140:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 24 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:	
ATGTTTTCA TCCTCACTTT TTGC	24
(2) INFORMATION FOR SEO ID NO:141:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:141:	
GGAGAAGAAC TGGAAGTTCA TC	22
(2) INFORMATION FOR SEO ID NO:142:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:	
ጥጥናል እጥርጥጥጥ A Aጥናጥጥጥናናናል ጥጥጥናር	25

(2) INFORMATION FOR SEO ID NO:143:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:143:	
TCTCCCACAG GTAATACTCC C	21
(2) INFORMATION FOR SEQ ID NO:144:	
(i) SEOUENCE CHARACTERISTICS: (A) LENGTH: 21 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:144:	
GCTACAACTG AATGGGGTAC G	21
(2) INFORMATION FOR SEO ID NO:145:	
(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 22 base pairs (B) TYPE: nucleic acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear	
(ii) MOLECULE TYPE: cDNA	
(vi) ORIGINAL SOURCE: (A) Homo sapiens	
(xi) SEQUENCE DESCRIPTION: SEO ID NO:145:	
CAGGACAAAA TAATCCTGTC CC	22
(2) INFORMATION FOR SEO ID NO:146:	

(i) SEQUENCE CHARACTERISTICS:					
(A) LENGTH: 24 base pair:	<u>s</u>				
(B) TYPE: nucleic acid					
(C) STRANDEDNESS: single					
(D) TOPOLOGY: linear					
(5) 10105001: 1111001					
(ii) MOLECULE TYPE: cDNA					
(vi) ORIGINAL SOURCE:					
(A) Homo sapiens					
(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:146:				
ATTTTCTTAC TTTCATTCTT CCTC					24
(2) INFORMATION FOR SEO ID NO:147:					
(i) SEQUENCE CHARACTERISTICS:					
(A) LENGTH: 20 amino acid	de .				
(B) TYPE: amino acid	<u> </u>				
(B) TIPE: amino acid					
(ii) MOLECULE TYPE: protein					
(vi) ORIGINAL SOURCE:					
(A) Artificial sequence	(concensus)				
(A) Altilitial sequence	(COMBENSUS)				
(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:147:				
Phe Xaa Val Glu Xaa Thr Pro Xaa Cys	Phe Ser Arg	Xaa Ser	Ser Leu	Ser	Ser Leu
1 5	10		15		
<u>Ser</u> 20					
(2) INFORMATION FOR SEQ ID NO:148:					
(i) SEQUENCE CHARACTERISTICS:					
(A) LENGTH: 20 amino acid	đe				
	<u>us</u>				
(B) TYPE: amino acid					
(ii) MOLECULE TYPE: protein					
(vi) ORIGINAL SOURCE:					
(A) Homo sapiens					
(11) 110110 3001 0119					
(xi) SEQUENCE DESCRIPTION: SEQ	ID NO:148:				
Tyr Cys Val Glu Asp Thr Pro Ile Cys	Phe Ser Arg	Cys Ser	Ser Lei	1	
1 5	10	_	15	_	
Ser Ser Leu Ser					

	20											
(2)	INFORMATION	FOR SE	O ID 1	NO:149	÷							
		NCE CHA LENGTH TYPE:	: 20 a	amino		<u>ls</u>						
	(ii) MOLEC	ULE TY	PE: pı	cotein								
	(vi) ORIGI	INAL SO Homo s		<u>5</u>								
	(xi) SEOUE	ENCE DE	SCRIPT	CION:	SEO	ID]	NO:1	<u> 49:</u>				
1	Thr Val Gln Ser Leu Asp	Glu Th	ır Pro	Leu M		Phe 10	Ser	Arg	Cys	Thr	Ser 15	Val
	20											
(2)	INFORMATION	FOR SE	0 ID 1	10:150	÷							
		NCE CHA LENGTH TYPE:	: 20 a	amino		<u>ls</u>						
	(ii) MOLEC	ULE TY	PE: pı	<u>rotein</u>	:							
	(vi) ORIGI	INAL SO Homo s		<u>5</u>								
	(xi) SEQUE	ENCE DE	SCRIPT	CION:	SEO	ID]	NO:1	<u>50:</u>				
Phe 1	Ala Thr Glu	Ser Th	ır Pro	Asp (Phe 10	Ser	Cys	Ser	Ser	Ser 15	Leu
	Ala Leu Ser 20					10					13	
(2)	INFORMATION	FOR SE	O ID 1	10:151	<u>:</u>							
		ICE CHA LENGTH TYPE:	: 20 8	amino		<u>ls</u>						
	(ii) MOLEC	CULE TY	PE: pi	rotein	L							
	(vi) ORIG	INAL SO Homo s	-	<u>s</u>								
	(xi) SEQUE	ENCE DE	SCRIP	rion:	SEO	ID :	NO:1	<u>51:</u>				
Tyr	Cys Val Glu	Gly Th	ır Pro	Ile A	Asn	Phe	Ser	Thr	Ala	Thr	Ser	Leu

1		5		10			<u>15</u>
	Asp Leu Thr						
501	20						
(2)	INFORMATION	FOR SEO I	D NO:152:	_			
	(i) SEOUEN						
		LENGTH: 2		acias			
	(B)	TYPE: ami	<u>ino acid</u>				
	(ii) MOLEC	ULE TYPE:	: protein				
	(vi) ORIGI						
	(A)	Homo sap	<u>lens</u>				
	(xi) SEOUE	ENCE DESCI	RIPTION:	SEO ID N	10:152:		
	1 01	GI Mb sa	Dec Bree (ive Dhe	Ser Ara	Asn Asp	Ser Leu
	Pro Ile Glu		Pro Tyr C	<u> 10</u>	Ser Arg	ZIDII TIDD	15
1		5		10			
Ser	Ser Leu Asp						
	20						
(2)	INFORMATION	FOR SEO	ID NO:153	<u>:</u>			
	(i) SEQUE	NCF CHARA	CTERTSTIC	S:			
		LENGTH:					
				<u>uozue</u>			
	(B)	TYPE: am	ino actu				
	(ii) MOLE	CULE TYPE	: protein	L			
	() ODIC	INAL SOUR	CE.				
	(A)	Homo sap	16115				
	(xi) SEOU	ENCE DESC	RIPTION:	SEO ID I	NO:153:		
Phe	e Ala Ile Glu	Asn Thr	Pro Val	Cys Pro	Ser His	Asn Ser	Ser Leu
1		5		10			<u>15</u>
	Ser Leu Ser						
<u> </u>	20	-					
(2)) INFORMATION	FOR SEQ	ID NO:154	<u>l:</u>			
			CONTROL CONT	ac.			
	(i) SEQUE						
		LENGTH:					
	(B)	TYPE: ar	nino acid				
	(ii) MOLE	ECULE TYPI	E: protei	<u>n</u>			
	(will Opto	GINAL SOU	RCE:				
) Homo sai					
	(A	I HOMO Sa	DTC119				
	(xi) SEO	UENCE DESC	CRIPTION:	SEO ID	NO:154:		

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Arq	His	Val	Glu	Asp	Thr	Pro	Val	Cys	Phe	Ser	Arg	Asn	Ser	Ser	Leu
1				5					10					15	
Ser	Ser	Leu	Ser												
			20												